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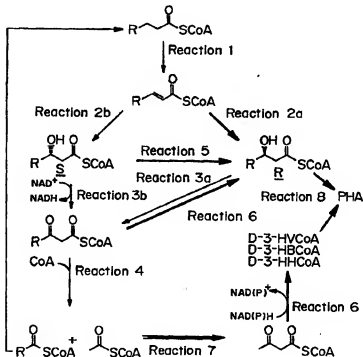
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(54) Title: MODIFICATION OF FATTY ACID METABOLISM IN PLANTS

**(57) Abstract**

Methods and systems to modify fatty acid biosynthesis and oxidation in plants to make new polymers are provided. Two enzymes are essential: a hydratase such as D-specific enoyl-CoA hydratase, for example, the hydratase obtained from *Aeromonas caviae*, and a  $\beta$ -oxidation enzyme system. Some plants have a  $\beta$ -oxidation enzyme system which is sufficient to modify polymer synthesis when the plants are engineered to express the hydratase. Examples demonstrate production of polymer by expression of these enzymes in transgenic plants. Examples also demonstrate that modifications in fatty acid biosynthesis can be used to modify plant phenotypes, decreasing or eliminating seed production and increasing green plant biomass, as well as producing polyhydroxylalkanones.



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## MODIFICATION OF FATTY ACID METABOLISM IN PLANTS

## Background Of The Invention

The present invention is generally in the field of transgenic plant systems for the production of polyhydroxyalkanoate materials, modification of triglycerides and fatty acids, and methods for altering seed production in plants.

Methods for producing stable transgenic plants for agronomic crops have been developed over the last 15 years. Crops have been genetically modified for improvements in both input and output traits. In the former traits, tolerance to specific agrochemicals has been engineered into crops, and specific natural pesticides, such as the *Bacillus thuringiensis* toxin, have been expressed directly in the plant. There also has been significant progress in developing male sterility systems for the production of hybrid plants. With respect to output traits, crops are being modified to increase the value of the product, generally the seed, grain, or fiber of the plant. Critical metabolic targets include the modification of starch, fatty acid, and oil biosynthetic pathways.

There is considerable commercial interest in producing microbial polyhydroxyalkanoate (PHA) biopolymers in plant crops. See, for example, U.S. Patent Nos. 5,245,023 and 5,250,430 to Peoples and Sinskey; U.S. Patent No. 5,502,273 to Bright et al.; U.S. Patent No. 5,534,432 to Peoples and Sinskey; U.S. Patent No. 5,602,321 to John; U.S. Patent No. 5,610,041 to Somerville et al.; PCT WO 91/00917; PCT WO 92/19747; PCT WO 93/02187; PCT WO 93/02194; PCT WO 94/12014; Poirier et al., *Science* 256:520-23 (1992); van der Leij & Witholt, *Can. J. Microbiol.* 41(supplement):222-38 (1995); Nawrath & Poirier, *The International Symposium on Bacterial Polyhydroxyalkanoates*, (Eggink et al., eds.) Davos Switzerland (August 18-23, 1996); and Williams and Peoples, *CHEMTECH* 26: 38-44 (1996). PHAs are natural, thermoplastic polyesters and can be processed by traditional polymer techniques for use in an enormous variety

of applications, including consumer packaging, disposable diaper linings and garbage bags, food and medical products.

Early studies on the production of polyhydroxybutyrate in the chloroplasts of the experimental plant system *Arabidopsis thaliana* resulted in the accumulation of up to 14% of the leaf dry weight as PHB (Nawrath et al., 1993). *Arabidopsis*, however, has no agronomic value. Moreover, in order to economically produce PHAs in agronomic crops, it is desirable to produce the PHAs in the seeds, so that the current infrastructure for harvesting and processing seeds can be utilized. The options for recovery of the PHAs from plant seeds (PCT WO 97/15681) and the end use applications (Williams & Peoples, CHEMTECH 26:38-44 (1996)) are significantly affected by the polymer composition. Therefore, it would be advantageous to develop transgenic plant systems that produce PHA polymers having a well-defined composition.

Careful selection of the PHA biosynthetic enzymes on the basis of their substrate specificity allows for the production of PHA polymers of defined composition in transgenic systems (U.S. Patent Nos. 5,229,279; 5,245,023; 5,250,430; 5,480,794; 5,512,669; 5,534,432; 5,661,026; and 5,663,063).

In bacteria, each PHA group is produced by a specific pathway. In the case of the short pendant group PHAs, three enzymes are involved:  $\beta$ -ketothiolase, acetoacetyl-CoA reductase, and PHA synthase. The homopolymer PHB, for example, is produced by the condensation of two molecules of acetyl-coenzyme A to give acetoacetyl-coenzyme A. The latter then is reduced to the chiral intermediate R-3-hydroxybutyryl-coenzyme A by the reductase, and subsequently polymerized by the PHA synthase enzyme. The PHA synthase notably has a relatively wide substrate specificity which allows it to polymerize C3-C5 hydroxy acid monomers including both 4-hydroxy and 5-hydroxy acid units. This biosynthetic pathway is found in a number of bacteria such as *Alcaligenes eutrophus*, *A. latus*, *Azotobacter vinlandii*, and *Zoogloea ramigera*. Long pendant group PHAs are produced for example by many different *Pseudomonas* bacteria.

Their biosynthesis involve the  $\beta$ -oxidation of fatty acids and fatty acid synthesis as routes to the hydroxyacyl-coenzyme A monomeric units. The latter then are converted by PHA synthases which have substrate specificities favoring the larger C6-C14 monomeric units (Peoples & Sinskey, 1990).

- 5 In the case of the PHB-co-HX copolymers which usually are produced from cells grown on fatty acids, a combination of these routes can be responsible for the formation of the different monomeric units. Indeed, analysis of the DNA locus encoding the PHA synthase gene in *Aeromonas caviae*, which produces the copolymer PHB-co-3-hydroxyhexanoate, was  
10 used to identify a gene encoding a D-specific enoyl-CoA hydratase responsible for the production of the D- $\beta$ -hydroxybutyryl-CoA and D- $\beta$ -hydroxyhexanoyl-CoA units (Fukui & Doi, *J. Bacteriol.* 179:4821-30 (1997); Fukui et. al., *J. Bacteriol.* 180:667-73 (1998)). Other sources of such hydratase genes and enzymes include *Alcaligenes*, *Pseudomonas*, and  
15 *Rhodospirillum*.

- The enzymes PHA synthase, acetoacetyl-CoA reductase, and  $\beta$ -ketothiolase, which produce the short pendant group PHAs in *A. eutrophus*, are coded by an operon comprising the *phbC-phbA-phbB* genes; Peoples et al., 1987; Peoples & Sinskey, 1989). In the *Pseudomonas* organisms, the  
20 PHA synthases responsible for production of the long pendant group PHAs have been found to be encoded on the *pha* locus, specifically by the *phaA* and *phaC* genes (U.S. Patent Nos. 5,245,023 and 5,250,430; Huisman et. al., *J. Biol. Chem.* 266:2191-98 (1991)). Since these earlier studies, a range of PHA biosynthetic genes have been isolated and characterized or identified  
25 from genome sequencing projects. Examples of known PHA biosynthetic genes are disclosed in the following references: *Aeromonas caviae* (Fukui & Doi, 1997, *J. Bacteriol.* 179:4821-30); *Alcaligenes eutrophus* (U.S. Patent Nos. 5,245,023; 5,250,430; 5,512,669; and 5,661,026; Peoples & Sinskey, *J. Biol. Chem.* 264:15298-03 (1989)); *Acinetobacter* (Schembri et. al., *FEMS Microbiol. Lett.* 118:145-52 (1994)); *Chromatium vinosum* (Liebergessel & Steinbuchel, *Eur. J. Biochem.* 209:135-50 (1992)); *Methylobacterium extorquens* (Valentin & Steinbuchel, *Appl. Microbiol. Biotechnol.* 39:309-17

- (1993)); *Nocardia corallina* (GENBANK Accession No. AF019964; Hall et al., 1998, *Can. J. Microbiol.* **44**:687-69); *Paracoccus denitrificans* (Ueda et al., *J. Bacteriol.* **178**:774-79 (1996); Yabutani et. al., *FEMS Microbiol. Lett.* **133**:85-90 (1995)); *Pseudomonas acidophila* (Umeda et. al., 1998, *Applied Biochemistry and Biotechnology*, **70-72**:341-52); *Pseudomonas sp.* 61-3 (Matsusaki et al., 1998, *J. Bacteriol.* **180**:6459-67); *Nocardia corallina*; *Pseudomonas aeruginosa* (Timm & Steinbuechel, *Eur. J. Biochem.* **209**:15-30 (1992)); *P. oleovorans* (U.S. Patent Nos. 5,245,023 and 5,250,430; Huisman et. al., *J. Biol. Chem.* **266**(4):2191-98 (1991); *Rhizobium etli* (Cevallos et. al., *J. Bacteriol.* **178**:1646-54 (1996)); *R. meliloti* (Tombolini et. al., *Microbiology* **141**:2553-59 (1995)); *Rhodococcus ruber* (Pieper-Furst & Steinbuechel, *FEMS Microbiol. Lett.* **75**:73-79 (1992)); *Rhodospirillum rubrum* (Hustede et. al., *FEMS Microbiol. Lett.* **93**:285-90 (1992)); *Rhodobacter sphaeroides* (Hustede et. al., *FEMS Microbiol. Rev.* **2**:217-30 (1992); *Biotechnol. Lett.* **15**:709-14 (1993); *Synechocystis sp.* (DNA Res. **3**:109-36 (1996)); *Thiopsis violacea* (*Appl. Microbiol. Biotechnol.* **38**:493-501 (1993)) and *Zoogloea ramigera* (Peoples et. al., *J. Biol. Chem.* **262**:97-102 (1987); Peoples & Sinskey, *Molecular Microbiology* **3**:349-57 (1989)). The availability of these genes or their published DNA sequences should provide a range of options for producing PHAs.

- PHA synthases suitable for producing PHB-co-HH copolymers comprising from 1-99% HH monomers are encoded by the *Rhodococcus ruber*, *Rhodospirillum rubrum*, *Thiopsis violacea*, and *Aeromonas caviae* PHA synthase genes. PHA synthases useful for incorporating 3-hydroxyacids of 6-12 carbon atoms in addition to R-3-hydroxybutyrate i.e. for producing biological polymers equivalent to the chemically synthesized copolymers described in PCT WO 95/20614, PCT WO 95/20615, and PCT WO 95/20621 have been identified in a number of *Pseudomonas* and other bacteria (Steinbuechel & Wiese, *Appl. Microbiol. Biotechnol.* **37**:691-97 (1992); Valentin et al., *Appl. Microbiol. Biotechnol.* **36**:507-14 (1992); Valentin et al., *Appl. Microbiol. Biotechnol.* **40**:710-16 (1994); Lee et al., *Appl. Microbiol. Biotechnol.* **42**:901-09 (1995); Kato et al., *Appl. Microbiol.*

- Biotechnol.* **45**:363-70 (1996); Abe et al., *Int. J. Biol. Macromol.* **16**:115-19 (1994); Valentin et al., *Appl. Microbiol. Biotechnol.* **46**:261-67 (1996)) and can readily be isolated as described in U.S. Patent Nos. 5,245,023 and 5,250,430. The PHA synthase from *P. oleovorans* (U.S. Patent Nos. 5,245,023 and 5,250,430; Huisman et. al., *J. Biol. Chem.* **266**(4): 2191-98 (1991)) is suitable for producing the long pendant group PHAs. Plant genes encoding  $\beta$ -ketothiolase also have been identified (Vollack & Bach, *Plant Physiol.* **111**:1097-107 (1996)).

- Despite this ability to modify monomer composition by selection of the syntheses and substrates, it is desirable to modify other features of polymer biosynthesis, such as that which involves fatty acid metabolism.

It is therefore an object of the present invention to provide a method and DNA constructs to introduce fatty acid oxidation enzyme systems for manipulating the cellular metabolism of plants.

- It is another object of the present invention to provide methods for enhancing the production of PHAs in plants, preferably in the oilseeds thereof.

#### Summary Of The Invention

- Methods and systems to modify fatty acid biosynthesis and oxidation in plants to make new polymers are described. Two enzymes are essential: a hydratase such as D-specific enoyl-CoA hydratase, for example, the hydratase obtained from *Aeromonas caviae*, and a  $\beta$ -oxidation enzyme system. Some plants have a  $\beta$ -oxidation enzyme system which is sufficient to modify polymer synthesis when the plants are engineered to express the hydratase.

- Examples demonstrate production of polymer by expression of these enzymes in transgenic plants. Examples also demonstrate that modifications in fatty acid biosynthesis can be used to alter plant phenotypes, decreasing or eliminating seed production and increasing green plant biomass, as well as producing PHAs.

### Brief Description of the Drawings

Figure 1 is a schematic of fatty acid  $\beta$ -oxidation routes to produce polyhydroxyalkanoate monomers.

Figure 2 is a schematic showing plasmid constructs pSBS2024 and  
5 pSBS2025.

Figures 3A and 3B are schematics showing plasmid constructs pCGmf124 and pCGmf125.

Figures 4A and 4B are schematics showing plasmid constructs pmf1249 and pmf1254.

10 Figures 5A and 5B are schematics showing plasmid constructs pCGmf224 and pCGmf225.

Figures 6A and 6B are schematics showing plasmid constructs pCGmf1P2S and pCGmf2P1S.

### Detailed Description Of The Invention

15 Methods and DNA constructs for manipulating the cellular metabolism of plants by introducing fatty acid oxidation enzyme systems into the cytoplasm or plastids of developing oilseeds or green tissue are provided. Fatty acid oxidation systems typically comprise several enzyme  
20 activities including a  $\beta$ -ketothiolase enzyme activity which utilizes a broad range of  $\beta$ -ketoacyl-CoA substrates.

It surprisingly was found that expression of at least one of these transgenes from the bean phaseolin promoter results in male sterility. Interestingly, these plants did not set seed, but instead produced higher than  
25 normal levels of biomass (e.g., leafs, stems, stalks). Therefore the methods and constructs described herein also can be used to create male sterile plants, for example, for hybrid production or to increase the production of biomass of forage, such as alfalfa or tobacco. Plants generated using these methods and DNA constructs are useful for producing polyhydroxyalkanoate  
30 biopolymers or for producing novel oil compositions.

The methods described herein include the subsequent incorporation of additional transgenes, in particular encoding additional enzymes involved



in fatty acid oxidation or polyhydroxyalkanoate biosynthesis. For polyhydroxyalkanoate biosynthesis, the methods include the incorporation of transgenes encoding enzymes, such as NADH and/or NADPH acetoacetyl-CoenzymeA reductases, PHB synthases, PHA synthases, acetoacetyl-CoA thiolase, hydroxyacyl-CoA epimerases, delta3-cis-delta2-trans enoyl-CoA isomerases, acyl-CoA dehydrogenase, acyl-CoA oxidase and enoyl-CoA hydratases by subsequent transformation of the transgenic plants produced using the methods and DNA constructs described herein or by traditional plant breeding methods.

#### 10 I. Plant Expression Systems

In a preferred embodiment, the fatty acid oxidation transgenes are expressed from a seed specific promoter, and the proteins are expressed in the cytoplasm of the developing oilseed. In an alternate preferred embodiment, fatty acid oxidation transgenes are expressed from a seed specific promoter and the expressed proteins are directed to the plastids using plastid targeting signals. In another preferred embodiment, the fatty acid oxidation transgenes are expressed directly from the plastid chromosome where they have been integrated by homologous recombination. The fatty acid oxidation transgenes may also be expressed throughout the entire plant tissue from a constitutive promoter. It is also useful to be able to control the expression of these transgenes by using promoters that can be activated following the application of an agrochemical or other active ingredient to the crop in the field. Additional control of the expression of these genes encompassed by the methods described herein include the use of recombination technologies for targeted insertion of the transgenes into specific chromosomal sites in the plant chromosome or to regulate the expression of the transgenes.

The methods described herein involve a plant seed having a genome including (a) a promoter operably linked to a first DNA sequence and a 3'-untranslated region, wherein the first DNA sequence encodes a fatty acid oxidation polypeptide and optionally (b) a promoter operably linked to a second DNA sequence and a 3'-untranslated region, wherein the second

DNA sequence encodes a fatty acid oxidation polypeptide. Expression of the two transgenes provides the plant with a functional fatty acid  $\beta$ -oxidation system having at least  $\beta$ -ketothiolase, dehydrogenase and hydratase activities in the cytoplasm or plastids other than peroxisomes or glyoxisomes. The first and/or second DNA sequence may be isolated from bacteria, yeast, fungi, algae, plants, or animals. It is preferable that at least one of the DNA sequences encodes a polypeptide with at least two, and preferably three, enzyme activities.

#### Transformation Vectors

DNA constructs useful in the methods described herein include transformation vectors capable of introducing transgenes into plants. Several plant transformation vector options are available, including those described in "Gene Transfer to Plants" (Potrykus, et al., eds.) Springer-Verlag Berlin Heidelberg New York (1995); "Transgenic Plants: A Production System for Industrial and Pharmaceutical Proteins" (Owen, et al., eds.) John Wiley & Sons Ltd. England (1996); and "Methods in Plant Molecular Biology: A Laboratory Course Manual" (Maliga, et al. eds.) Cold Spring Laboratory Press, New York (1995). Plant transformation vectors generally include one or more coding sequences of interest under the transcriptional control of 5' and 3' regulatory sequences, including a promoter, a transcription termination and/or polyadenylation signal, and a selectable or screenable marker gene. The usual requirements for 5' regulatory sequences include a promoter, a transcription termination and/or a polyadenylation signal. For the expression of two or more polypeptides from a single transcript, additional RNA processing signals and ribozyme sequences can be engineered into the construct (U.S. Patent No. 5,519,164). This approach has the advantage of locating multiple transgenes in a single locus, which is advantageous in subsequent plant breeding efforts. An additional approach is to use a vector to specifically transform the plant plastid chromosome by homologous recombination (U.S. Patent No. 5,545,818), in which case it is possible to take advantage of the prokaryotic nature of the plastid genome and insert a number of transgenes as an operon.

### Promoters

- A large number of plant promoters are known and result in either constitutive, or environmentally or developmentally regulated expression of the gene of interest. Plant promoters can be selected to control the
- 5 expression of the transgene in different plant tissues or organelles for all of which methods are known to those skilled in the art (Gasser & Fraley, *Science* 244:1293-99 (1989)). The 5' end of the transgene may be engineered to include sequences encoding plastid or other subcellular organelle targeting peptides linked in-frame with the transgene. Suitable
- 10 constitutive plant promoters include the cauliflower mosaic virus 35S promoter (CaMV) and enhanced CaMV promoters (Odell et. al., *Nature*, 313: 810 (1985)), actin promoter (McElroy et al., *Plant Cell* 2:163-71 (1990)), AdhI promoter (Fromm et. al., *Bio/Technology* 8:833-39 (1990); Kyozuka et al., *Mol. Gen. Genet.* 228:40-48 (1991)), ubiquitin promoters, the
- 15 Figwort mosaic virus promoter, mannopine synthase promoter, nopaline synthase promoter and octopine synthase promoter. Useful regulatable promoter systems include spinach nitrate-inducible promoter, heat shock promoters, small subunit of ribulose biphosphate carboxylase promoters and chemically inducible promoters (U.S. Patent No. 5,364,780 to Hershey et
- 20 al.).

- In a preferred embodiment of the methods described herein, the transgenes are expressed only in the developing seeds. Promoters suitable for this purpose include the napin gene promoter (U.S. Patent Nos. 5,420,034 and 5,608,152), the acetyl-CoA carboxylase promoter (U.S. Patent Nos.
- 25 5,420,034 and 5,608,152), 2S albumin promoter, seed storage protein promoter, phaseolin promoter (Slightom et. al., *Proc. Natl. Acad. Sci. USA* 80:1897-1901 (1983)), oleosin promoter (Plant et. al., *Plant Mol. Biol.* 25:193-205 (1994); Rowley et al., *Biochim. Biophys. Acta.* 1345:1-4 (1997); U.S. Patent No. 5,650,554; and PCT WO 93/20216), zein promoter, glutelin
- 30 promoter, starch synthase promoter, and starch branching enzyme promoter.

The transformation of suitable agronomic plant hosts using these vectors can be accomplished with a variety of methods and plant tissues.

Representative plants useful in the methods disclosed herein include the *Brassica* family including *napus*, *rappa*, *sp. carinata* and *juncea*; maize; soybean; cottonseed; sunflower; palm; coconut; safflower; peanut; mustards including *Sinapis alba*; and flax. Crops harvested as biomass, such as silage

corn, alfalfa, or tobacco, also are useful with the methods disclosed herein.

Representative tissues for transformation using these vectors include protoplasts, cells, callus tissue, leaf discs, pollen, and meristems.

Representative transformation procedures include *Agrobacterium*-mediated transformation, biolistics, microinjection, electroporation, polyethylene

glycol-mediated protoplast transformation, liposome-mediated transformation, and silicon fiber-mediated transformation (U.S. Patent No.

5,464,765; "Gene Transfer to Plants" (Potrykus, et al., eds.) Springer-Verlag Berlin Heidelberg New York (1995); "Transgenic Plants: A Production

System for Industrial and Pharmaceutical Proteins" (Owen, et al., eds.) John

Wiley & Sons Ltd. England (1996); and "Methods in Plant Molecular Biology: A Laboratory Course Manual" (Maliga, et al. eds.) Cold Spring Laboratory Press, New York (1995)).

## II. Methods for Making and Screening for Transgenic Plants

In order to generate transgenic plants using the constructs described

herein, the following procedures can be used to obtain a transformed plant expressing the transgenes subsequent to transformation: select the plant cells that have been transformed on a selective medium; regenerate the plant cells that have been transformed to produce differentiated plants; select transformed plants expressing the transgene at such that the level of desired polypeptide is obtained in the desired tissue and cellular location.

For the specific crops useful for practicing the described methods, transformation procedures have been established, as described for example, in "Gene Transfer to Plants" (Potrykus, et al., eds.) Springer-Verlag Berlin Heidelberg New York (1995); "Transgenic Plants: A Production System for Industrial and Pharmaceutical Proteins" (Owen, et al., eds.) John Wiley & Sons Ltd. England (1996); and "Methods in Plant Molecular Biology: A Laboratory Course Manual" (Maliga, et al. eds.) Cold Spring Laboratory

Press, New York (1995).

- Brassica napus* can be transformed as described, for example, in U.S. Patent Nos. 5,188,958 and 5,463,174. Other *Brassica* such as *rappa*, *carinata* and *junceae* as well as *Sinapis alba* can be transformed as described
- 5 by Moloney et. al., *Plant Cell Reports* 8:238-42 (1989). Soybean can be transformed by a number of reported procedures (U.S. Patent Nos. 5,015,580; 5,015,944; 5,024,944; 5,322,783; 5,416,011; and 5,169,770). Several transformation procedures have been reported for the production of transgenic maize plants including pollen transformation (U.S. Patent No.
- 10 5,629,183), silicon fiber-mediated transformation (U.S. Patent No. 5,464,765), electroporation of protoplasts (U.S. Patent Nos. 5,231,019; 5,472,869; and 5,384,253) gene gun (U.S. Patent Nos. 5,538,877 and 5,538,880 and *Agrobacterium*-mediated transformation (EP 0 604 662 A1; PCT WO 94/00977). The *Agrobacterium*-mediated procedure is particularly
- 15 preferred, since single integration events of the transgene constructs are more readily obtained using this procedure, which greatly facilitates subsequent plant breeding. Cotton can be transformed by particle bombardment (U.S. Patent Nos. 5,004,863 and 5,159,135). Sunflower can be transformed using a combination of particle bombardment and *Agrobacterium* infection (EP 0
- 20 486 233 A2; U.S. Patent No. 5,030,572). Flax can be transformed by either particle bombardment or *Agrobacterium*-mediated transformation. Recombinase technologies include the *cre-lox*, FLP/FRT, and Gin systems. Methods for utilizing these technologies are described for example in U.S. Patent No. 5,527,695 to Hodges et al.; Dale & Ow, *Proc. Natl. Acad. Sci.*
- 25 *USA* 88:10558-62 (1991); Medberry et. al., *Nucleic Acids Res.* 23:485-90 (1995).

#### Selectable Marker Genes

- Selectable marker genes useful in practicing the methods described herein include the neomycin phosphotransferase gene *nptII* (U.S. Patent Nos.
- 30 5,034,322 and 5,530,196), hygromycin resistance gene (U.S. Patent No. 5,668,298), *bar* gene encoding resistance to phosphinothricin (U.S. Patent No. 5,276,268). EP 0 530 129 A1 describes a positive selection system

which enables the transformed plants to outgrow the non-transformed lines by expressing a transgene encoding an enzyme that activates an inactive compound added to the growth media. Screenable marker genes useful in the methods herein include the  $\beta$ -glucuronidase gene (Jefferson et. al., *EMBO J.* 6:3901-07 (1987); U.S. Patent No. 5,268,463) and native or modified green fluorescent protein gene (Cubitt et. al., *Trends Biochem Sci.* 20:448-55 (1995); Pang et. al., *Plant Physiol.* 112:893-900 (1996)). Some of these markers have the added advantage of introducing a trait, such as herbicide resistance, into the plant of interest, thereby providing an additional agronomic value on the input side.

In a preferred embodiment of the methods described herein, more than one gene product is expressed in the plant. This expression can be achieved via a number of different methods, including (1) introducing the encoding DNAs in a single transformation event where all necessary DNAs are on a single vector; (2) introducing the encoding DNAs in a co-transformation event where all necessary DNAs are on separate vectors but introduced into plant cells simultaneously; (3) introducing the encoding DNAs by independent transformation events successively into the plant cells i.e. transformation of transgenic plant cells expressing one or more of the encoding DNAs with additional DNA constructs; and (4) transformation of each of the required DNA constructs by separate transformation events, obtaining transgenic plants expressing the individual proteins and using traditional plant breeding methods to incorporate the entire pathway into a single plant.

### III. $\beta$ -Oxidation Enzyme Pathways

Production of PHAs in the cytosol of plants requires the cytosolic localization of enzymes that are able to produce R-3-hydroxyacyl CoA thioesters as substrates for PHA synthases. Both eukaryotes and prokaryotes possess a  $\beta$ -oxidation pathway for fatty acid degradation that consists of a series of enzymes that convert fatty acyl CoA thioesters to acetyl CoA. While these pathways proceed via intermediate 3-hydroxyacyl CoA, the stereochemistry of this intermediate varies among organisms. For example,

the  $\beta$ -oxidation pathways of bacteria and the peroxisomal pathway of higher eukaryotes degrade fatty acids to acetyl CoA via S-3-hydroxyacyl CoA (Schultz, "Oxidation of Fatty Acids" in *Biochemistry of Lipids, Lipoproteins and Membranes* (Vance et al., eds.) pp. 101-06 (Elsevier, Amsterdam 1991)).

- 5 In *Escherichia coli*, an epimerase activity encoded by the  $\beta$ -oxidation multifunctional enzyme complex is capable of converting S-3-hydroxyacyl CoA to R-3-hydroxyacyl CoA. Yeast possesses a peroxisomal localized fatty acid degradation pathway that proceeds via intermediate R-3-hydroxyacyl CoA (Hiltunen, et al. *J. Biol. Chem.* 267: 6646-53 (1992);
- 10 Filppula, et al. *J. Biol. Chem.* 270:27453-57 (1995)), such that no epimerase activity is required to produce PHAs.

- Plants, like other higher eukaryotes, possesses a  $\beta$ -oxidation pathway for fatty acid degradation localized subcellularly in the peroxisomes (Gerhardt, "Catabolism of Fatty Acids [ $\alpha$  and  $\beta$  Oxidation]" in *Lipid*
- 15 *Metabolism in Plants* (Moore, Jr., ed.) pp. 527-65 (CRC Press, Boca Raton, Florida 1993)). Production of PHAs in the cytosol of plants therefore necessitates the cytosolic expression of a  $\beta$ -oxidation pathway, for conversion of fatty acids to R-3-hydroxyacyl CoA thioesters of the correct chain length, as well as cytosolic expression of an appropriate PHA synthase,
- 20 to polymerize R-3-hydroxyacyl CoA to polymer.

- Fatty acids are synthesized as saturated acyl-ACP thioesters in the plastids of plants (Hartwood, "Plant Lipid Metabolism" in *Plant Biochemistry* (Dey et al., eds.) pp. 237-72 (Academic Press, San Diego 1997)). Prior to export from the plastid into the cytosol, the majority of fatty
- 25 acids are desaturated via a  $\Delta 9$  desaturase. The pool of newly synthesized fatty acids in most oilseed crops consists predominantly of oleic acid (*cis* 9-octadecenoic acid), stearic acid (octadecanoic acid), and palmitic acid (hexadecanoic acid). However, some plants, such as coconut and palm kernel, synthesize shorter chain fatty acids (C8-14). The fatty acid is
- 30 released from ACP via a thioesterase and subsequently converted to an acyl-CoA thioester via an acyl CoA synthetase located in the plastid membrane (Andrews, et al., "Fatty acid and lipid biosynthesis and degradation" in *Plant*

*Physiology, Biochemistry, and Molecular Biology* (Dennis et al., eds.) pp. 345-46 (Longman Scientific & Technical, Essex, England 1990); Harwood, "Plant Lipid Metabolism" in *Plant Biochemistry* (Dey et al., eds) p. 246 (Academic Press, San Diego 1997)).

- 5       The cytosolic conversion of the pool of newly synthesized acyl CoA thioesters via fatty acid degradation pathways and the conversion of intermediates from these series of reactions to R-3-hydroxyacyl-CoA substrates for PHA synthases can be achieved via the enzyme reactions outlined in Figure 1. The PHA synthase substrates are C4-C16 R-3-
- 10   hydroxyacyl CoAs. For saturated fatty acyl CoAs, conversion to R-3-hydroxyacyl CoA thioesters using fatty acids degradation pathways necessitates the following sequence of reactions: conversion of the acyl CoA thioester to *trans*-2-enoyl-CoA (reaction 1), hydration of *trans*-2-enoyl-CoA to R-3-hydroxy acyl CoA (reaction 2a, e.g. yeast system operates through
- 15   this route and the *Aeromonas caviae* D-specific hydratase yields C4-C7 R-3-hydroxyacyl-CoAs), hydration of *trans*-2-enoyl-CoA to S-3-hydroxy acyl CoA (reaction 2b), and epimerization of S-3-hydroxyacyl CoA to R-3-hydroxyacyl CoA (reaction 5, e.g. cucumber tetrafunctional protein, bacterial systems). If 3-hydroxyacyl CoA is not polymerized by PHA synthase
- 20   forming PHA, it can proceed through the remainder of the  $\beta$ -oxidation pathway as follows: oxidation of 3-hydroxyacyl CoA to form  $\beta$ -keto acyl CoA (reaction 3) followed by thiolysis in the presence of CoA to yield acetyl CoA and a saturated acyl CoA thioester shorter by two carbon units (reaction 4). The acyl CoA thioester produced in reaction 4 is free to re-enter the  $\beta$ -
- 25   oxidation pathway at reaction 1 and the acetyl-CoA produced can be converted to R-3-hydroxyacyl CoA by the action of  $\beta$ -ketothiolase (reaction 7) and NADH or NADPH acetoacetyl-CoA reductase (reaction 6). This latter route is useful for producing R-3-hydroxybutyryl-CoA, R-3-hydroxyvaleryl-CoA and R-3-hydroxyhexanoyl-CoA. The R-3-
- 30   hydroxyacids of four to sixteen carbon atoms produced by this series of enzymatic reactions can be polymerized by PHA synthases expressed from a transgene, or transgenes in the case of the two subunit synthase enzymes,



into PHA polymers.

- For  $\Delta 9$  unsaturated fatty acyl CoAs, a variation of the reaction sequences described is required. Three cycles of  $\beta$ -oxidation, as detailed in Figure 1, will remove six carbon units yielding an unsaturated acyl CoA thioester with a *cis* double bond at position 3. Conversion of the *cis* double bond at position 3 to a *trans* double bond at position 2, catalyzed by  $\Delta^3$ -*cis*- $\Delta^2$ -*trans*-enoyl CoA isomerase will allow the  $\beta$ -oxidation reaction sequences outlined in Figure 1 to proceed. This enzyme activity is present on the microbial  $\beta$ -oxidation complexes and the plant tetrafunctional protein, but not on the yeast *fox1*.

Acyl CoA thioesters also can be degraded to a  $\beta$ -keto acyl CoA and converted to R-3-hydroxyacyl CoA via a NADH or NADPH dependent reductase (reaction 6).

- Multifunctional enzymes that encode S-specific hydratase, S-specific dehydrogenase,  $\beta$ -ketothiolase, epimerase and  $\Delta^3$ -*cis*- $\Delta^2$ -*trans*-enoyl CoA isomerase activities have been found in bacteria such as *Escherichia coli* (Spratt, et al., *J. Bacteriol.* 158:535-42 (1984)) and *Pseudomonas fragi* (Immure, et al., *J. Biochem.* 107:184-89 (1990)). The multifunctional enzyme complexes consist of two copies of each of two subunits such that catalytically active protein forms a heterotetramer. The hydratase, dehydrogenase, epimerase, and  $\Delta^3$ -*cis*- $\Delta^2$ -*trans*-enoyl CoA isomerase activities are located on one subunit, whereas the thiolase is located on another subunit. The genes encoding the enzymes from organisms such as *E. coli* (Spratt, et al., *J. Bacteriol.* 158:535-42 (1984); DiRusso, *J. Bacteriol.* 172:6459-68 (1990)) and *P. fragi* (Sato, et al., *J. Biochem.* 111:8-15 (1992)) have been isolated and sequenced and are suitable for practicing the methods described herein. Furthermore, the *E. coli* enzyme system has been subjected to site-directed mutagenesis analysis to identify amino acid residues critical to the individual enzyme activities (He & Yang, *Biochemistry* 35:9625-30 (1996); Yang et. al., *Biochemistry* 34:6641-47 (1995); He & Yang, *Biochemistry* 36:11044-49 (1997); He et. al., *Biochemistry* 36:261-68 (1997); Yang & Elzinga, *J. Biol. Chem.* 268:6588-

92 (1993)). These mutant genes also could be used in some embodiments of the methods described herein.

- Mammals, such as rat, possess a trifunctional  $\beta$ -oxidation enzyme in their peroxisomes that contains hydratase, dehydrogenase, and  $\Delta^3$ -*cis*- $\Delta^2$ -*trans*-enoyl CoA isomerase activities. The trifunctional enzyme from rat liver has been isolated and has been found to be monomeric with a molecular weight of 78 kDa (Palosaari, et al., *J. Biol. Chem.* 265:2446-49 (1990)). Unlike the bacterial system, thiolase activity is not part of the multienzyme protein (Schultz, "Oxidation of Fatty Acids" in *Biochemistry of Lipids, Lipoproteins and Membranes* (Vance et al., eds) p. 95 (Elsevier, Amsterdam (1991)). Epimerization in rat occurs by the combined activities of two distinct hydratases, one which converts R-3-hydroxyacyl CoA to *trans*-2-enoyl CoA, and another which converts *trans*-2-enoyl CoA to S-3-hydroxyacyl CoA (Smeland, et al., *Biochemical and Biophysical Research Communications* 160:988-92 (1989)). Mammals also possess  $\beta$ -oxidation pathways in their mitochondria that degrade fatty acids to acetyl CoA via intermediate S-3-hydroxyacyl CoA (Schultz, "Oxidation of Fatty Acids" in *Biochemistry of Lipids, Lipoproteins and Membranes* (Vance et al., eds) p. 96 (Elsevier, Amsterdam (1991)). Genes encoding mitochondrial  $\beta$ -oxidation activities have been isolated from several animals including a Rat mitochondrial long chain acyl CoA hydratase/3-hydroxy acyl CoA dehydrogenase (GENBANK Accession # D16478) and a Rat mitochondrial thiolase (GENBANK Accession #s D13921, D00511).

- Yeast possesses a multifunctional enzyme, Fox2, that differs from the  $\beta$ -oxidation complexes of bacteria and higher eukaryotes in that it proceeds via a R-3-hydroxyacyl CoA intermediate instead of S-3-hydroxyacyl CoA (Hiltunen, et al., *J. Biol. Chem.* 267:6646-53 (1992)). Fox2 possesses R-specific hydratase and R-specific dehydrogenase enzyme activities. This enzyme does not possess the  $\Delta^3$ -*cis*- $\Delta^2$ -*trans*-enoyl CoA isomerase activity needed for degradation of  $\Delta^9$ -*cis*-hydroxyacyl CoAs to form R-3-hydroxyacyl CoAs. The gene encoding fox2 from yeast has been isolated and sequenced and encodes a 900 amino acid protein. The DNA sequence of

the structural gene and amino acid sequence of the encoded polypeptide is shown in SEQ ID NO:1 and SEQ ID NO:2.

- Plants have a tetrafunctional protein similar to the yeast Fox2, but also encoding a  $\Delta^3$ -*cis*- $\Delta^2$ -*trans*-enoyl CoA isomerase activity (Muller et., al.,  
5 *J. Biol. Chem.* 269:20475-81 (1994)). The DNA sequence of the cDNA and amino acid sequence of the encoded polypeptide is shown in SEQ ID NO:3 and SEQ ID NO:4.

#### IV. Targeting of Enzymes to the Cytoplasm of Oil Seed Crops

- Engineering PHA production in the cytoplasm of plants requires  
10 directing the expression of  $\beta$ -oxidation to the cytosol of the plant. No targeting signals are present in the bacterial systems, such as faoAB. In fungi, yeast, plants, and mammals,  $\beta$ -oxidation occurs in subcellular organelles. Typically, the genes are expressed from the nuclear chromosome, and the polypeptides synthesized in the cytoplasm are directed  
15 to these organelles by the presence of specific amino acid sequences. To practice the methods described herein using genes isolated from eukaryotic sources, e.g., fatty acid oxidation enzymes from eukaryotic sources, such as yeast, fungi, plants, and mammals, the removal or modification of subcellular targeting signals is required to direct the enzymes to the cytosol.  
20 It may be useful to add signals for directing proteins to the endoplasmic reticulum. Peptides useful in this process are well known in the art. The general approach is to modify the transgene by inserting a DNA sequence specifying an ER targeting peptide sequence to form a chimeric gene.

- Eukaryotic acyl CoA dehydrogenases, as well as other mitochondrial  
25 proteins, are targeted to the mitochondria via leader peptides on the N-terminus of the protein that are usually 20-60 amino acids long (Horwich, *Current Opinion in Cell Biology*, 2:625-33 (1990)). Despite the lack of an obvious consensus sequence for mitochondrial import leader peptides, mutagenesis of key residues in the leader sequence have been demonstrated  
30 to prevent the import of the mitochondrial protein. For example, the import of *Saccharomyces cerevisiae* F1-ATPase was prevented by mutagenesis of its leader sequence, resulting in the accumulation of the modified precursor

protein in the cytoplasm (Bedwell, et al., *Mol. Cell Biol.* 9:1014-25 (1989))

Three eukaryotic peroxisomal targeting signals have been reported (Gould, et al., *J. Cell Biol.* 108:1657-64 (1989); Brickner, et al., *J. Plant Physiol.*, 113:1213-21 (1997)). The tripeptide targeting signal S/A/C-

- 5 K/H/R-L occurs at the C-terminal end of many peroxisomal proteins (Gould, et al., *J. Cell Biol.* 108:1657-64 (1989)). Mutagenesis of this sequence has been shown to prevent import of proteins into peroxisomes. Some peroxisomal proteins do not contain the tripeptide at the C-terminal end of the protein. For these proteins, it has been suggested that targeting occurs
- 10 via the tripeptide in an internal position within the protein sequence (Gould, et al., *J. Cell Biol.* 108:1657-64 (1989)) or via an unknown, unrelated sequence (Brickner, et al., *J. Plant Physiol.* 113:1213-21 (1997)). The results of *in vitro* peroxisomal targeting experiments with fragments of acyl CoA oxidase from *Candida tropicalis* appear to support the latter theory and
- 15 suggest that there are two separate targeting signals within the internal amino acid sequence of the polypeptide (Small, et al., *The EMBO Journal* 7:1167-73 (1988)). In the aforementioned study, the targeting signals were localized to two regions of 118 amino acids in length, and neither of regions was found to contain the targeting signal S/A/C-K/H/R-L. A small number of
- 20 peroxisomal proteins appear to contain an amino terminal leader sequence for import into peroxisomes (Brickner, et al., *J. Plant Physiol.* 113:1213-21 (1997)). These targeting signals can be deleted or altered by site directed mutagenesis.

#### V. Cultivation and Harvesting of Transgenic Plant

- 25 The transgenic plants can be grown using standard cultivation techniques. The plant or plant part also can be harvested using standard equipment and methods. The PHAs can be recovered from the plant or plant part using known techniques such as solvent extraction in conjunction with traditional seed processing technologies, as described in PCT WO 97/15681,
- 30 or can be used directly, for example, as animal feed, where it is unnecessary to extract the PHA from the plant biomass.

Several lines which did not produce seed, produced much higher

levels of biomass. produced much higher levels of biomass. This phenotype therefore may be useful as a means to increase the amount of green biomass produced per acre for silage, forage, or other biomass crops. End uses include the more cost effective production of forage crops for animal feed or  
5 as energy crops for electric power generation. Other uses include increasing biomass levels in crops, such as alfalfa or tobacco, for subsequent recovery of industrial products, such as PHAs by extraction.

The compositions and methods of preparation and use thereof described herein are further described by the following non-limiting  
10 examples.

**Example 1: Isolation and Characterization of the *Pseudomonas putida* *faoAB* Genes and Fao Enzyme**

All DNA manipulations, including PCR, DNA sequencing *E. coli* transformation, and plasmids purification, were performed using standard  
15 procedures, as described, for example, by Sambrook et. al., Molecular Cloning: A Laboratory Manual (Cold Spring Harbor Laboratory Press, New York (1989)). The genes encoding *faoAB* from *Pseudomonas putida* were isolated using a probe generated from *P. putida* genomic DNA by PCR  
20 (polymerase chain reaction) using primers 1 and 2 possessing homology to *faoB* from *Pseudomonas fragi* (Sato, et al., *J. Biochem.* 111:8-15 (1992)).

Primer 1:

5' gat ggg ccg ctc caa ggg tgg 3' (SEQ ID NO:5)

Primer 2:

25 5' caa ccc gaa ggt gcc gcc att 3' (SEQ ID NO:6)

A 1.1 kb DNA fragment was purified from the PCR reaction and used as a probe to screen a *P. putida* genomic library constructed in plasmid pBKCMV using the lambda ZAP expression system (Stratagene). Plasmid pMFX1 was selected from the positive clones and the DNA sequence of the  
30 insert containing the *faoAB* genes and flanking sequences determined. This is shown in SEQ ID NO:7. A fragment containing *faoAB* was subcloned with the native *P. putida* ribosome binding site intact into the expression

vector pTRCN forming plasmid pMFX3 as follows. Plasmid pMFX1 was digested with *Bsr*G I. The resulting protruding ends were filled in with Klenow. Digestion with *Hind* III yielded a 3.39 kb blunt ended/*Hind* III fragment encoding FaoAB. The expression vector pTRCN was digested with *Sma* I/*Hind* III and ligated with the *faoAB* fragment forming the 7.57 kb plasmid pMFX3.

Enzymes in the FaoAB multienzyme complex were assayed as follows. Hydratase activity was assayed by monitoring the conversion of NAD to NADH using the coupling enzyme L- $\beta$ -hydroxyacyl CoA dehydrogenase as previously described, except that assays were run in the presence of CoA (Filppula, et al., *J. Biol. Chem.* 270:27453-57 (1995)). Severe product inhibition of the coupling enzyme was observed in the absence of CoA. The assay contained (1 mL final volume) 60  $\mu$ M crotonyl CoA, 50  $\mu$ M Tris-Cl, pH 9, 50  $\mu$ g bovine serum albumin per mL, 50 mM KCl, 1 mM NAD, 7  $\mu$ g L-specific  $\beta$ -hydroxyacyl CoA dehydrogenase from porcine heart per mL, and 0.25 mM CoA. The assay was initiated with the addition of FaoAB to the assay mixture. A control assay was performed without substrate to determine the rate of consumption of NAD in the absence of the hydratase generated product, S-hydroxybutyryl CoA. One unit of activity is defined as the consumption of one  $\mu$ Mol of NAD per min ( $\epsilon_{340} = 6220 \text{ M}^{-1}\text{cm}^{-1}$ ).

Hydroxyacyl CoA dehydrogenase was assayed in the reverse direction with acetoacetyl CoA as the substrate by monitoring the conversion of NADH to NAD at 340 nm (Binstock, et al., *Methods in Enzymology*, 71:403 (1981)). The assay contained (1 mL final volume) 0.1 M  $\text{KH}_2\text{PO}_4$ , pH 7, 0.2 mg bovine serum albumin per mL, 0.1 mM NADH, and 33  $\mu$ M acetoacetyl CoA. The assay was initiated with the addition of FaoAB to the assay mixture. When necessary, enzyme samples were diluted in 0.1 M  $\text{KH}_2\text{PO}_4$ , pH 7, containing 1 mg bovine serum albumin per mL. A control assay was performed without substrate acetoacetyl CoA to detect the rate of consumption of NADH in the crude due to enzymes other than hydroxyacyl CoA dehydrogenase. One unit of activity is defined as the consumption of

one  $\mu\text{Mol}$  of NADH per minute ( $\epsilon_{340} = 6220 \text{ M}^{-1}\text{cm}^{-1}$ ).

- HydroxyacylCoA dehydrogenase was assayed in the forward direction with crotonyl CoA as a substrate by monitoring the conversion of NAD to NADH at 340 nm (Binstock, et al., *Methods in Enzymology*, **71**:403 (1981)). The assay mixture contained (1 mL final volume) 0.1 M  $\text{KH}_2\text{PO}_4$ , pH 8, 0.3 mg bovine serum albumin per mL, 2 mM  $\beta$ -mercaptoethanol, 0.25 mM CoA, 30  $\mu\text{M}$  crotonyl CoA, and an aliquot of FaoAB. The reaction was preincubated for a couple of minutes to allow *in situ* formation of S-hydroxybutyryl CoA. The assay then was initiated by the addition of NAD (0.45 mM). A control assay was performed without substrate to detect the rate of consumption of NAD due to enzymes other than hydroxyacyl CoA dehydrogenase. One unit of activity is defined as the consumption of one  $\mu\text{Mol}$  of NAD per minute ( $\epsilon_{340} = 6220 \text{ M}^{-1}\text{cm}^{-1}$ ).

- Thiolase activity was determined by monitoring the decrease in absorption at 304 nm due to consumption of substrate acetoacetyl CoA as previously described with some modifications (Palmer, et al., *J. Biol. Chem.* **266**:1-7 (1991)). The assay contained (final volume 1 mL) 62.4 mM Tris-Cl, pH 8.1, 4.8 mM  $\text{MgCl}_2$ , 62.5  $\mu\text{M}$  CoA, and 62.5  $\mu\text{M}$  acetoacetyl CoA. The assay was initiated with the addition of FaoAB to the assay mixture. A control sample without enzyme was performed for each assay to detect the rate of substrate degradation of pH 8.1 in the absence of enzyme. One unit of activity is defined as the consumption of one  $\mu\text{Mol}$  of substrate acetoacetyl CoA per minute ( $\epsilon_{340} = 16900 \text{ M}^{-1}\text{cm}^{-1}$ ).

- Epimerase activity was assayed as previously described (Binstock, et al., *Methods in Enzymology*, **71**:403 (1981)) except that R-3-hydroxyacyl CoA thioesters were utilized instead of D,L-3-hydroxyacyl CoA mixtures. The assay contained (final volume 1 mL) 30  $\mu\text{M}$  R-3-hydroxyacyl CoA, 150 mM  $\text{KH}_2\text{PO}_4$  (pH 8), 0.3 mg/mL BSA, 0.5 mM NAD, 0.1 mM CoA, and 7  $\mu\text{g/mL}$  L-specific  $\beta$ -hydroxyacyl CoA dehydrogenase from porcine heart. The assay was initiated with the addition of FaoAB.

For expression of FaoAB in DH5 $\alpha$ /pMFX3, cultures were grown in 2xTY medium at 30 °C. 2xTY medium contains (per L) 16 g tryptone, 10 g

yeast, and 5 g NaCl. A starter culture was grown overnight and used to inoculate (1% inoculum) fresh medium (100 mL in a 250 mL Erlenmeyer flask for small scale growths; 1.5L in a 2.8L flask for large scale growths). Cells were induced with 0.4 mM IPTG when the absorbance at 600 nm was in the range of 0.4 to 0.6. Cells were cultured an additional 4 h prior to harvest. Cells were lysed by sonication, and the insoluble matter was removed from the soluble proteins by centrifugation. Acyl CoA dehydrogenase activity was monitored in the reverse direction to ensure activity of the FaoA subunit (SEQ ID NO:31) and thiolase activity was assayed to determine activity of the Fao subunit. FaoAB in DH5 $\alpha$ /pMFX3 contained dehydrogenase and thiolase activity values of 4.3 and 0.99 U/mg, respectively, which is significantly more than the 0.0074 and 0.0033 U/mg observed for dehydrogenase and thiolase, respectively, in control strain DH5 $\alpha$ /pTRCN.

FaoAB was purified from DH5 $\alpha$ /pMFX3 using a modified procedure previously described for the purification of FaoAB from *Pseudomonas fragi* (Imamura, et al., *J. Biochem.* 107:184-89 (1990)). Thiolase activity (assayed in the forward direction) and dehydrogenase activities (assayed in the reverse direction) were monitored throughout the purification. Three liters of DH5 $\alpha$ /pMFX3 cells (2 X 1.5 L aliquots in 2.8 L Erlenmeyer flasks) were grown in 2 x TY medium using the cell growth procedure previously described for preparing cells for enzyme activity analysis. Cells (15.8 g) were resuspended in 32 mL of 10 mM KH<sub>2</sub>PO<sub>4</sub>, pH 7, and lysed by sonication. Soluble proteins were removed from insoluble cells debris by centrifugation (18,000 RPM, 30 min., 4 °C). The soluble extract was made 50% in acetone and the precipitated protein was isolated by centrifugation and redissolved in 10 mM KH<sub>2</sub>PO<sub>4</sub>, pH 7. The sample was adjusted to 33% saturation with (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub> and the soluble and insoluble proteins were separated by centrifugation. The resulting supernatant was adjusted to 56% saturation with (NH<sub>4</sub>)<sub>2</sub>SO<sub>4</sub> and the insoluble pellet was isolated by centrifugation and dissolved in 10 mM KH<sub>2</sub>PO<sub>4</sub>, pH 7. The sample was heated at 50°C for 30 min. and the soluble proteins were isolated by



centrifugation and dialyzed in a 6,000 to 8,000 molecular weight cut off membrane in 10 mM  $\text{KH}_2\text{PO}_4$ , pH 7 (2 X 3L; 20 h). The sample was loaded on a Toyo Jozo DEAE FPLC column (3 cm x 14 cm) that previously had been equilibrated in 10 mM  $\text{KH}_2\text{PO}_4$ , pH 7. The protein was eluted with a linear gradient (100 mL by 100 mL; 0 to 500 mM NaCl in 10  $\text{KH}_2\text{PO}_4$ , pH 7) at a flow of 3 mL/min. FaoAB eluted between 300 and 325 mM NaCl. The sample was dialyzed in a 50,000 molecular weight cut off membrane in 10 mM  $\text{KH}_2\text{PO}_4$ , pH 7 (1 X 2L; 15h) prior to loading on a macro-prep hydroxylapatite 18/30 (Biorad) FPLC column (2 cm x 15 cm) that previously had been equilibrated in 10 mM  $\text{KH}_2\text{PO}_4$ , pH 7. The protein was eluted with a linear gradient (250 mL by 250 mL; 10 to 500 mM  $\text{KH}_2\text{PO}_4$ , pH 7) at a flow rate of 3 mL/min. FaoAB eluted between 70 and 130 mM  $\text{KH}_2\text{PO}_4$ . The fractions containing activity were concentrated to 9 mL using a MILLIPORE<sup>TM</sup> 100,000 molecular weight cutoff concentrator. The buffer was exchanged 3 times with 10 mM  $\text{KH}_2\text{PO}_4$ , pH 7 containing 20% sucrose and frozen at -70°C. Enzyme activities of the hydroxylapatite purified fraction were assayed with a range of substrates. The results are shown in Table 1 below.

Table 1: Enzyme Substrates and Activities

Enzyme	Substrate	Activity (U/mg)
hydratase	crotonyl CoA	8.8
dehydrogenase (forward)	crotonyl CoA	0.46
dehydrogenase (reverse)	acetoacetyl CoA	29
thiolase	acetoacetyl CoA	9.9
epimerase	R-3-hydroxyoctanoyl CoA	0.022
epimerase	R-3- hydroxyhexanoyl CoA	0.0029
epimerase	R-3- hydroxybutyryl CoA	0.000022

#### Example 2: Production of Antibodies to the FaoAB and FaoAB Polypeptides

Following purification of the FaoAB protein as described in Example 1, a sample was separated by SDS-PAGE. The protein band corresponding to the FaoA (SEQ ID NO:31) and FaoB (SEQ ID NO:26) was excised and used to immunize New Zealand white rabbits with complete Freund's adjuvant. Boosts were performed using incomplete Freund's at three week

intervals. Antibodies were recovered from serum by affinity chromatography on Protein A columns (Pharmacia) and tested against the antigen by Western blotting procedures. Control extracts of *Brassica* seeds were used to test for cross reactivity to plant proteins. No cross reactivity was detected.

**Example 3: Construction of Plasmids for Expression of the  
*Pseudomonas putida* *fao* AB Genes in Transgenic Oilseeds**  
Construction of pSBS2024

- 10 Oligonucleotide primers GVR471  
5'-CGGTACCCATTGTACTCCAGTATCAT-3' (SEQ ID NO:8)  
and GVR472  
5'-CATTAAATAGTAGAGTATTGAATATG-3' (SEQ ID NO:9)  
homologous to sequences flanking the 5' and 3' ends (underlined),  
15 respectively, of the bean phaseolin promoter (SEQ ID NO:10; Slightom *et al.*, 1983) were designed with the addition of *Kpn*I (in italics, nucleotides 1-7 in SEQ ID NO:8) and *Sma*I (in italics, nucleotides 1-9 in SEQ ID NO:9) at the 5' ends of GVR471 and GVR472, respectively. These restriction sites were incorporated to facilitate cloning. The primers were used to amplify a  
20 1.4 kb phaseolin promoter, which was cloned at the *Sma*I site in pUC19 by blunt ended ligation. The designated plasmid, pCPPI (see Figure 2) was cut with *Sal*I and *Sma*I and ligated to a *Sal*I/*Sma*I phaseolin terminator (SEQ ID NO:27). The bean phaseolin terminator sequence encompassing the polyadenylation signals was amplified using the following PCR primers:  
25 GVR396:  
5'-GATTTAAATGCAAGCTTAAATAAGTATGAACTAAAATGC-3'  
(SEQ ID NO:22)  
and GVR397:  
5'-CGGTACCTTAGTTGGTAGGGTGCTA-3' (SEQ ID NO:23)  
30 and the 1.2Kb fragment (SEQ ID NO:27) cloned into *Sal*I-*Sal*I site of pCCPI to obtain pSBS2024 (Figure 2). The resulting plasmid which contains a unique *Hind*III site for cloning was called pSBS2024 (Figure 2).

Construction of pSBS2025

A soybean oleosin promoter fragment (SEQ ID NO:11; Rowley *et al.*, 1997) was simplified with primers that flank the DNA sequence.

Primer JA408

- 5        5' -TCTAGATACATCCATTTCCTTAATATAATCCTCTTATTC-3'  
           (SEQ ID NO:12)

contains sequences that are complementary to the 5' end (underlined).

Primer np1

- 5' -CATTTAAATGGTTAAGGTGAAGGTAGGGCT-3'  
 10        (SEQ ID NO:13)

contains sequences homologous to the 3' end (underlined) of the promoter fragment. The restriction sites *Xba*I (in italics) and *Swa*I (in italics) were incorporated at the 5' end of JA408 and np1, respectively, to facilitate cloning. The primers were used to amplify a 975 bp promoter fragment, which then was cloned into *Sma*II site of pUC19 (see Figure 2). The resulting plasmid, pCSP1, was cut with *Sa*II and *Swa*I and ligated to the soybean terminator (SEQ ID NO:28). The soybean oleosin terminator was amplified by PCR using the following primers:

JA410:

- 20        5'-AAGCTTACGTGATGAGTATTAATGTGTTGTTATG-3'  
           (SEQ ID NO:29)

and

JA411:

- 5'-TCTAGACAATTCATCAAATACAAATCACATTGCC-3'  
 25        (SEQ ID NO:30)

and the 225 bp fragment cloned into the *Sa*II-*Swa*I site of pCSP1 to obtain plasmid pSBS2025 (Figure 6). The designated plasmid, pSBS2025, carried a unique *Hind*III site for cloning (Figure 2).

Construction of Promoter-coding Sequence Fusions

Two oligonucleotide primers were synthesized:

np2

5' AAGCTTAAAATGATTACGAAGGTAAAGCC-3'

5 (SEQ ID NO:14)

homologous to nucleotides 553 to 573 of the 5' flanking sequences, and

np3

5' ATTGCTTTCAGTTGAAGCGCTG-3'

(SEQ ID NO:15)

10 complementary to nucleotides 2700 to 2683 flanking the 3' end of mfl (faoA, SEQ ID NO:24) of plasmid pmfx3. A *HindIII* (in italics) site was introduced at the 5' end of primers np2 and np3 to facilitate cloning. In addition, a 3 bp AAA sequence (bold) was incorporated to obtain a more favorable sequence surrounding the plant translational initiation codon. Primers np2 and np3  
15 were used to amplify the fragment and cloned into *SmaI* site of pUC19. The resulting plasmid was called pCmfl (Figures 3A and 3B). Plasmid pBmf2 was constructed in a similar process (Figures 5A and 5B). In order to generate a *HindIII* (in italics) at 5' and 3' ends of the mfl (faoB) gene (SEQ ID NO:25) for cloning, a second set of synthetic primers were designed.

20 Primers np4

5' -AAGCTTAAAATGAGCCTGAATCCAAGAGAC-3'

(SEQ ID NO:16)

complementary to 5' (nucleotides 2732-2752 bp) and np5

5' AAGCTTTCAGACGCGTTTCGAAGACAGTG-3'

25 (SEQ ID NO:17)

homologous to 3' (nucleotides 3907-3886 bp) sequences of mfl2 (faoB, SEQ ID NO:25) of plasmid pmfx3 were used in a PCR reaction to amplify the 1.17 kb DNA fragment. The resulting PCR product was cloned into the *EcoRV* site of pBluescript. The plasmid was referred to as pBmf2.

30 Both plasmids were individually cut with *HindIII* and their inserts cloned in plasmids pSBS2024 and pSBS2025, which had previously been linearized with the same restriction enzyme. As a result, the following

- plasmids were generated: pmf124 and pmf125 (Figures 3A and 3B) and pmf224 and pmf225 (Figures 5A and 5B) containing the Fao genes (mf1 and mf2) fused to either the phaseolin or soybean promoters. DNA sequence analysis confirmed the correct promoter-coding sequence-termination
- 5 sequence fusions for pmf124, pmf125, pmf224, and pmf225.

**Example 4: Assembly of Promoter-coding Sequence  
Fusions into Plant Transformation Vectors**

- After obtaining plasmids pmf124, pmf125, pmf224, and pmf225,
- 10 promoter-coding sequence fusions were independently cloned into the binary vectors, pCGN1559 (McBride and Summerfelt, 1990) containing the CaMV 35S promoter driving the expression of NPTII gene (conferring resistance to the antibiotic kanamycin) and pSBS2004 containing a parsley ubiquitin promoter driving the PPT gene, which confers resistance to the herbicide
- 15 phosphinothricine. Binary vectors suitable for this purpose with a variety of selectable markers can be obtained from several sources.

- The phaseolin-mf21 fusion cassette was released from the parent plasmid with *Xba*I and ligated with pCGN1559, which had been linearized with the same restriction enzyme. The resulting plasmid was designated
- 20 pCGmf124 (Figures 3A and 3B). Plasmid pCGmf125 containing the soybean-mf1 fusion was constructed in a similar way (Figures 3A and 3B), except that both pmf125 and pCGN1559 were cut with *Bam*HI before ligation.

Construction of pmf1249 and pmf1254

- 25 The plasmid pSBS2004 was linearized with *Bam*HI fragment containing the soybean-mf1 fusion. This plasmid was designated pmf1254 (Figures 4A and 4B). Similarly, the *Xba*I phaseolin-mf1 fusion fragment was ligated to pSBS2004 which had been linearized with the same restriction enzyme. The resulting plasmid was designated pmf1249 (Figures 4A and
- 30 4B).

Construction of pCGmf224 and pCGmf225

The phaseolin-mf2 and soybean-mf2 fusions were constructed by

excising the fusions from the vector by cutting with either *Bam*HI or *Xba*I, and cloned into pCGN1559 which had been linearized with either restriction enzyme (Figures 5A and 5B).

#### Construction of pCGmf1P2S and pCGmf2P1S

- 5           The two expression cassettes containing the promoter-coding sequence fusions were assembled on the same binary vector as follows: Plasmid pmf124 containing the phaseolin-mf1 fusion was cut with *Bam*HI and cloned into the *Bam*HI site of pCGN1559 to create pCGmfB124. This plasmid then was linearized with *Xba*I and ligated to the *Xba*I fragment of
- 10 pmf225 containing the soybean-mf2 fusion. The final plasmid was designated pCGmf1P2S (Figures 6A and 6B). Plasmid pCGmf2P1S was assembled in similar manner. The phaseolin-mf2 fusion was released from pmf224 by cutting with *Bam*HI and cloned at the *Bam*HI site of pCGN1559. The resulting plasmid, pCGmfB224, was linearized with *Xba*I and ligated to
- 15 the *Xba*I fragment of pmf125 containing the soybean-mf1 fusion (Figures 6A and 6B).

#### **Example 5: Transformation of *Brassica***

- Brassica* seeds were surface sterilized in 10% commercial bleach
- 20 (Javex, Colgate-Palmolive) for 30 min. with gentle shaking. The seeds were washed three times in sterile distilled water. Seeds were placed in germination medium comprising Murashige-Skoog (MS) salts and vitamins, 3% (w/v) sucrose and 0.7% (w/v) phytagar, pH 5.8 at a density of 20 per plate and maintained at 24 °C and a 16 h light / 8 h dark photoperiod at a
- 25 light intensity of 60-80  $\mu\text{Em}^{-2}\text{s}^{-1}$  for four to five days.

- Each of the constructs, pCGmf124, pCGmf125, pCGmf224, pCGmf1P2S, and pCGmf2P1S were introduced into *Agrobacterium tumefaciens* strain EHA101 (Hood et al., *J. Bacteriol.* 168:1291-1301 (1986)) by electroporation. Prior to transformation of cotyledonary petioles,
- 30 single colonies of strain EHA101 harboring each construct were grown in 5 ml of minimal medium supplemented with 100 mg kanamycin per liter and 100 mg gentamycin per liter for 48 hr at 28 °C. One milliliter of bacterial

suspension was pelleted by centrifugation for 1 min in a microfuge. The pellet was resuspended in 1 ml minimal medium.

For transformation, cotyledons were excised from 4 day old, or in some cases 5 day old, seedlings, so that they included approximately 2 mm of petiole at the base. Individual cotyledons with the cut surface of their petioles were immersed in diluted bacterial suspension for 1 s and immediately embedded to a depth of approximately 2 mm in co-cultivation medium, MS medium with 3% (w/v) sucrose and 0.7% phytagar and enriched with 20  $\mu$ M benzyladenine. The inoculated cotyledons were plated at a density of 10 per plate and incubated under the same growth conditions for 48 h. After co-cultivation, the cotyledons then were transferred to regeneration medium comprising MS medium supplemented with 3% sucrose, 20  $\mu$ M benzyladenine, 0.7% (w/v) phytagar, pH 5.8, 300 mg timentinin per liter, and 20 mg kanamycin sulfate per liter.

After two to three weeks, regenerant shoots obtained were cut and maintained on "shoot elongation" medium (MS medium containing, 3% sucrose, 300 mg timentin per liter, 0.7% (w/v) phytagar, 300 mg timentinin per liter, and 20 mg kanamycin sulfate per liter, pH 5.8) in Magenta jars. The elongated shoots were transferred to "rooting" medium comprising MS medium, 3% sucrose, 2 mg indole butyric acid per liter, 0.7% phytagar, and 500 mg carbenicillin per liter. After roots emerged, plantlets were transferred to potting mix (Redi Earth, W.R. Grace and Co.). The plants were maintained in a misting chamber (75% relative humidity) under the same growth conditions. Two to three weeks after growth, leaf samples were taken for neomycin phosphotransferase (NPTII) assays (Moloney et al., *Plant Cell Reports* 8:238-42 (1989)).

Seeds from the FaoA and FaoB transgenic lines can be analyzed for expression of the fatty acid oxidation polypeptides by western blotting using the anti-FaoA and anti-FaoB antibodies. The FaoB polypeptide (SEQ ID NO:26) is not functional in the absence of the FaoA gene product; however, the FaoAB gene product has enzyme activity.

Transgenic lines expressing the FaoA and FaoB complex are obtained

by crossing the FaoA and FaoB transgenic lines expressing the individual polypeptides and seeds analyzed by western blotting and enzymes assays as described.

5   **Example 6: Transformation of *B. napus* cv. Westar  
and Analysis of Transgenic Lines**

Transformation

The protocol used was adopted from a procedure described by  
Moloney *et al.* (1989). Seeds of *Brassica napus* cv. Westar were surface  
10   sterilized in 10% commercial bleach (Javex, Colgate-Palmolive Canada Inc.)  
for 30 min with gentle shaking. The seeds were washed three times in sterile  
distilled water. Seeds were placed on germination medium comprising  
Murashige-Skoog (MS) salts and vitamins, 3% sucrose and 0.7% phytagar,  
pH 5.8 at a density of 20 per plate and maintained at 24 °C in a 16 h light/8  
15   h dark photoperiod at a light intensity of 60-80  $\mu\text{Em}^{-2}\text{s}^{-1}$  for four to five days.

Each of the constructs, pCGmf124, pCGmf125, pCGmf224,  
pCGmf225, pCGmf1P2S, and pCGmf2P1S were introduced into  
*Agrobacterium tumefaciens* strain EHA101 (Hood *et al.* 1986) by  
electroporation. Prior to transformation of cotyledonary petioles, single  
20   colonies of strain EHA101 harboring each construct were grown in 5 mL of  
minimal medium supplemented with 100 mg kanamycin per liter, and 100  
mg gentamycin per liter for 48 h at 28 °C. One milliliter of bacterial  
suspension was pelleted by centrifugation for 1 min in a microfuge. The  
pellet was resuspended in 1 mL minimal medium.

25   For transformation, cotyledons were excised from four-day-old, or in  
some cases five-day-old, seedlings so that they included approximately 2 mm  
of petiole at the base. Individual cotyledons with the cut surface of their  
petioles were immersed in diluted bacterial suspension for 1 s and  
immediately embedded to a depth of approximately 2 mm in co-cultivation  
30   medium, MS medium with 3% sucrose and 0.7% phytagar, enriched with 20  
 $\mu\text{M}$  benzyladenine. The inoculated cotyledons were plated at a density of 10  
per plate and incubated under the same growth conditions for 48 h. After



co-cultivation, the cotyledons then were transferred to regeneration medium, which comprised MS medium supplemented with 3% sucrose, 20  $\mu$ M benzyladenine, 0.7% phytagar, pH 5.8, 300 mg timentinin per liter, and 20 mg kanamycin sulfate per liter.

- 5 After two to three weeks, regenerant shoots were obtained, cut, and maintained on "shoot elongation" medium (MS medium containing 3% sucrose, 300mg timentin per liter, 0.7% phytagar, and 20 mg kanamycin per liter, pH 5.8) in Magenta jars. The elongated shoots then were transferred to "rooting" medium, which comprised MS medium, 3% sucrose, 2 mg indole
- 10 butyric acid per liter, 0.7% phytagar and 500 mg carbenicillin per liter. After roots emerged, the plantlets were transferred to potting mix (Redi Earth, W.R. Grace and Co. Canada Ltd.). The plants were maintained in a misting chamber (75% RH) under the same growth conditions. Two to three weeks after growth, leaf samples were taken for neomycin phosphotransferase
- 15 (NPT II) assays (Moloney *et al.* 1989). The results are shown in Table 2 below. The data show the number of plants that were confirmed to be transformed.

**Table 2: NPT II Activity in Transformed Plants**

Constructs	No. of plants	NPTII assayed	NPTII confirmed	No. of plants confirmed transformed
<sup>1</sup> pCGmf124	47	27	23	33
<sup>2</sup> pCGmf125	37	28	18	18
<sup>3</sup> pCGmf224	49	40	30	39
<sup>4</sup> pCGmf225	52	37	28	34
<sup>5</sup> pCGmf1P2S	27	27	21	21
<sup>6</sup> pCGmf2P1S				

- 20 <sup>1</sup>pCGmf124 – bean phaseolin regulatory sequences driving FaoA gene  
<sup>2</sup>pCGmf125 – soybean oleosin regulatory sequences driving FaoA gene  
<sup>3</sup>pCGmf224 – bean phaseolin regulatory sequences driving FaoB gene  
<sup>4</sup>pCGmf225 – soybean oleosin regulatory sequences driving FaoB gene  
<sup>5</sup>pCGmf1P2S – bean phaseolin and soybean oleosin regulatory sequences driving FaoA & FaoB genes, respectively  
 25 <sup>6</sup>pCGmf2P1S – bean phaseolin and soybean oleosin regulatory sequences driving FaoB & FaoA genes, respectively

- The fate of the transforming DNA was investigated for sixteen randomly selected transgenic lines. Southern DNA hybridization analysis
- 30 showed that the FaoA and/or FaoB were integrated into the genomes of the

transgenic lines tested.

Approximately 80% of the pmf124 transgenic plants in which the FaoA gene is expressed from the strong bean phaseolin promoter were observed to be male sterile. Clearly high level expression of the FaoA gene from this promoter results in functional expression of the FaoA gene product which impairs seed and/or pollen development. This result was very unexpected, since it was not anticipated that the plant cells would be capable of carrying out the first step in the  $\beta$ -oxidation pathway in the cytosol. This result, however, provides additional applications for expressing  $\beta$ -oxidation genes in plants for male sterility for hybrid production or to prevent the production of seed. It was also noted that in a side-by-side comparison with normal transgenic lines, the pmf124 lines produced much higher levels of biomass, presumably due to the elimination of seed development. This phenotype therefore may be useful as a means to increase the amount of green biomass produced per acre for silage, forage, or other biomass crops. Here, the use of an inducible promoter system or recombinase technology could be used to produce seed for planting. Seven of the sterile plants were successfully cross-pollinated with pollen from pmf225 transgenic lines and set seeds.

Northern analysis on RNA from seeds from pmf224 lines containing the phaseolin promoter-FaoB constructs showed a signal indicative of the expected 1.2 kb transcript in all the samples tested except the control. Northern analysis on RNA from seeds from pmf125 lines containing the weak soybean oleosin promoter-FaoA constructs revealed a transcript of the expected size of 2.1 kb. Western blotting on 300-500  $\mu$ g of protein from approximately 80% of seeds of pmf125 plants where the FaoA gene is expressed from the relatively weak soybean oleosin promoter were inconclusive, although a weak signal was detected in one transgenic line.

Fatty Acid Analysis

Given the unexpected results indicating a strong metabolic effect of expressing the FaoA gene from the strong bean phaseolin promoter in seeds, the fatty acid profile of the seeds from transgenic lines expressing the FaoA

gene from the weak soybean oleosin promoter was analyzed. Seeds expressing only the FaoA gene or also expressing the FaoB gene from the bean phaseolin promoter were examined. The analysis was carried out as described in Millar et al., *The Plant Cell* 11:1889-902 (1998). Seed fatty acid methyl esters (FAMES) were prepared by placing ten seeds of *B. napus* in 15 x 45-mm screw capped glass tubes and heating at 80 °C in 0.75 mL of 1N methanolic HCl reagent (Supelco, PA) and 10 µL of 1 mg 17:0 methyl ester (internal standard) per mL overnight. After cooling the samples, the FAMES were extracted with 0.3 mL hexane and 0.5 mL 0.9% NaCl by vortexing vigorously. The samples were allowed to stand to separate the phases, and 300 µL of the organic phase was drawn and analyzed on a Hewlett-Packard gas chromatograph.

Fatty acid profile analysis indicated the presence of an additional component or enhanced component in the lipid profile in all of the transgenic plants expressing the FaoA gene SEQ ID NO:24 which was absent from the control plants. This result again proves conclusively that the FaoA gene is being transcribed and translated and that the FaoA polypeptide SEQ ID NO: 27 is catalytically active. This peak also was observed in eleven additional transgenic plants harboring SoyP-FaoA, PhaP-FaoA-SoyP-FaoB, SoyP-FaoA-PhaP-FaoB genes and a sterile (PhaP-FaoA) plant cross-pollinated with SoyP-FaoB. These data clearly demonstrate functional expression of the FaoA gene and that even the very low levels of expression are sufficient to change the lipid profile of the seed. Adapting the methods described herein, one of skill in the art can express these genes at levels intermediate between that obtained with the phaseolin promoter and the soybean oleosin promoter using other promoters such as the *Arabidopsis oleosin* promoter, napin promoter, or cruciferin promoter, and can use inducible promoter systems or recombinase technologies to control when fatty acid oxidation transgenes are expressed.

#### Example 7: Yeast $\beta$ -oxidation Multi-functional Enzyme Complex

*S. cerevisiae* contains a  $\beta$ -oxidation pathway that proceeds via R-

hydroxyacyl CoA rather than the S-3-hydroxyacyl CoA observed in bacteria and higher eukaryotes. The *fox2* gene from yeast encodes a hydratase that produces R-3-hydroxyacyl CoA from *trans*-2-enoyl-CoA and a dehydrogenase that utilizes R-3-hydroxyacyl-CoA to produce  $\beta$ -keto acyl

5 CoAs.

The *fox2* gene (sequence shown in SEQ ID NO:1) was isolated from *S. cerevisiae* genomic DNA by PCR in two pieces. Primers N-fox2b and N-bamfox2b were utilized to PCR a 1.1 kb SmaI/BamHI fragment encoding the N-terminal region of Fox2, and primers C-fox2 and C-bamfox2 were utilized  
15 to PCR a 1.6 kb BamHI/XbaI fragment encoding the C-terminal Fox2 region. The full *fox2* gene was reconstructed via subcloning in vector pTRCN.

N-fox2b fox2

tcc ccc ggg agg agg ttt tta tta tgc ctg gaa att tat cct tca aag ata gag tt  
15 (SEQ ID NO:18)

N-bamfox2b fox2

aaggatccttgatgtcattacaactacc (SEQ ID NO:19)

C-fox2 fox2

gct cta gat agg gaa aga tgt atg taa g (SEQ ID NO:20)

20 C-bamfox2 fox2

tgacatcaaggatcctttt (SEQ ID NO:21)

The *fox1* gene, however, does not possess a  $\beta$ -ketothiolase activity and this activity must be supplied by a second transgene. Representative sources of such a gene include algae, bacteria, yeast, plants, and mammals. The  
25 bacterium *Alcaligenes eutrophus* possesses a broad specificity  $\beta$ -ketothiolase gene suitable for use in the methods described herein. It can be readily isolated using the acetoacetyl-CoA thiolase gene as a hybridization probe, as described in U.S. Patent 5,661,026 to Peoples et al. This enzyme also has been purified (Haywood et al., *FEMS Micro. Lett.* 52:91 (1988)), and the  
30 purified enzyme is useful for preparing antibodies or determining protein sequence information as a basis for the isolation of the gene.

**Example 8: Plant  $\beta$ -Oxidation Gene**

The DNA sequence of the cDNA encoding  $\beta$ -oxidation tetrafunctional protein, shown in SEQ ID NO:4, can be isolated as described in Preisig-Muller et al., *J. Biol. Chem.* 269:20475-81 (1994). The equivalent  
5 gene can be isolated from other plant species including *Arabidopsis*,  
*Brassica*, soybean, sunflower, and corn using similar procedures or by screening genomic libraries, many of which are commercially available, for example from Clontech Laboratories Inc., Palo Alto, California, USA. A peroxisomal targeting sequence P-R-M was identified at the carboxy  
10 terminus of the protein. Constructs suitable for expressing in the plant cytosol can be prepared by PCR amplification of this gene using primers designed to delete this sequence.

We claim:

1. A method for manipulating the metabolism of a plant, comprising expressing heterologous genes encoding fatty acid oxidation enzymes in cytosol or plastids other than the peroxisomes, glyoxisomes or mitochondria of the plant.
2. The method of claim 1 wherein the fatty acid  $\beta$ -oxidation enzymes are expressed from genes selected from the group consisting of bacterial, yeast, fungal, plant, and mammalian.
3. The method of claim 2 wherein the fatty acid oxidation enzymes are expressed from genes from bacteria selected from the group consisting of *Escherichia*, *Pseudomonas*, *Alcaligenes*, and *Coryneform*.
4. The method claim 3 wherein the genes are *Pseudomonas putida faoAB*.
5. The method of claim 1 further comprising expressing genes encoding enzymes selected from the group consisting of polyhydroxyalkanoate synthases, acetoacetyl-CoA reductases,  $\beta$ -ketoacyl-CoA thiolases, and enoyl-CoA hydratases.
6. A DNA construct for use in a method of manipulating the metabolism of a plant cell comprising, in phase,
  - (a) a promoter region functional in a plant;
  - (b) a structural DNA sequence encoding at least one fatty acid oxidation enzyme activity; and
  - (c) a 3' nontranslated region of a gene naturally expressed in a plant, wherein the nontranslated region encodes a signal sequence for polyadenylation of mRNA.
7. The DNA construct of claim 6 wherein the promoter is a seed specific promoter.
8. The DNA construct of claim 7 wherein the seed specific promoter is selected from the group consisting of napin promoter, phaseolin promoter, oleosin promoter, 2S albumin promoter, zein promoter,  $\beta$ -conglycinin promoter, acyl-carrier protein promoter, and fatty acid desaturase promoter.

9. The DNA construct of claim 6 wherein the promoter is a constitutive promoter.

10. The DNA construct of claim 6 wherein the promoter is selected from the group consisting of CaMV 35S promoter, enhanced CaMV 35S promoter, and ubiquitin promoter.

11. A method for enhancing the biological production of polyhydroxyalkanoates in a transgenic plant, comprising  
expressing genes encoding heterologous fatty acid oxidation enzymes in cytosol or plastids other than the peroxisomes, glyoxisomes or mitochondria of the plant.

12. The method of claim 11 wherein the transgenic plant is selected from the group consisting of *Brassica*, maize, soybean, cottonseed, sunflower, palm, coconut, safflower, peanut, mustards, flax, tobacco, and alfalfa.

13. A transgenic plant or part thereof comprising  
heterologous genes encoding fatty acid oxidation enzymes in cytosol or plastids other than the peroxisomes, glyoxisomes or mitochondria of the plant.

14. The plant or part thereof of claim 13 wherein the fatty acid  $\beta$ -oxidation enzymes are expressed from genes selected from the group consisting of bacterial, yeast, fungal, plant, and mammalian.

15. The plant or part thereof of claim 14 wherein the fatty acid oxidation enzymes are expressed from genes from bacteria selected from the group consisting of *Escherichia*, *Pseudomonas*, *Alcaligenes*, and *Coryneform*.

16. The plant or part thereof of claim 15 wherein the genes are *Pseudomonas putida faoAB*.

17. The plant or part thereof of claim 13 further comprising  
genes encoding enzymes selected from the group consisting of polyhydroxyalkanoate synthases, acetoacetyl-CoA reductases,  $\beta$ -ketoacyl-CoA thiolases, and enoyl-CoA hydratases.

18. The plant or part thereof of claim 13 wherein the plant is selected from the group consisting of *Brassica*, maize, soybean, cottonseed, sunflower, palm, coconut, safflower, peanut, mustards, flax, tobacco, and alfalfa.

19. The plant or part thereof comprising a DNA construct comprising, in phase,

(a) a promoter region functional in a plant;

(b) a structural DNA sequence encoding at least one fatty acid oxidation enzyme activity; and

(c) a 3' nontranslated region of a gene naturally expressed in a plant, wherein the nontranslated region encodes a signal sequence for polyadenylation of mRNA.

20. The plant or part thereof of claim 19 wherein the promoter is a seed specific promoter.

21. The plant or part thereof of claim 20 wherein the seed specific promoter is selected from the group consisting of napin promoter, phaseolin promoter, oleosin promoter, 2S albumin promoter, zein promoter,  $\beta$ -conglycinin promoter, acyl-carrier protein promoter, and fatty acid desaturase promoter.

22. The plant or part thereof of claim 19 wherein the promoter is a constitutive promoter.

23. The plant or part thereof of claim 20 wherein the promoter is selected from the group consisting of CaMV 35S promoter, enhanced CaMV 35S promoter, and ubiquitin promoter.

24. A method of preventing or suppressing seed production in a plant, comprising

expressing heterologous genes encoding fatty acid oxidation enzymes in cytosol or plastids other than the peroxisomes, glyoxisomes or mitochondria of the plant.



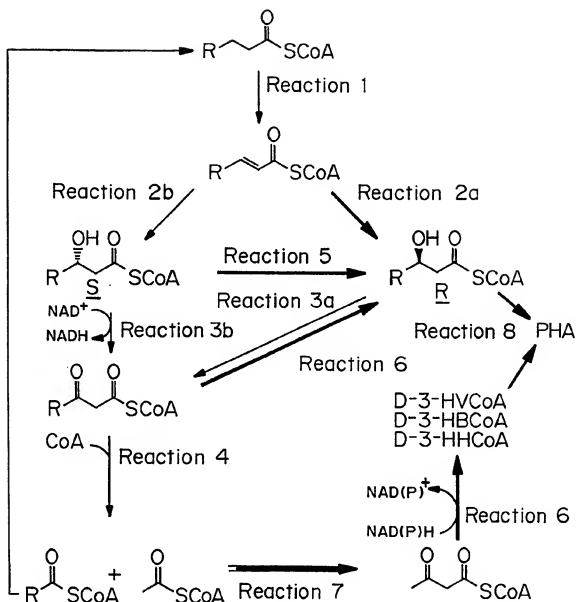


FIG. 1

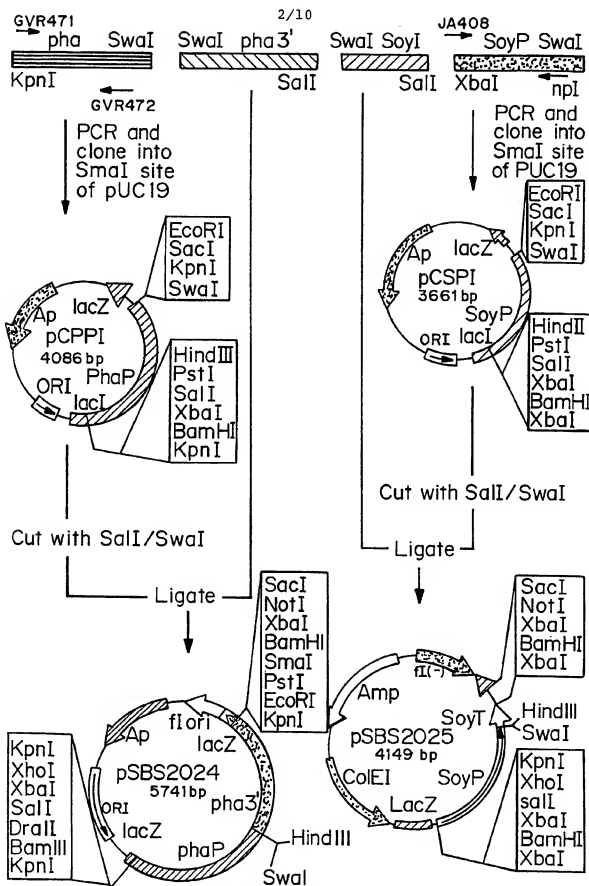
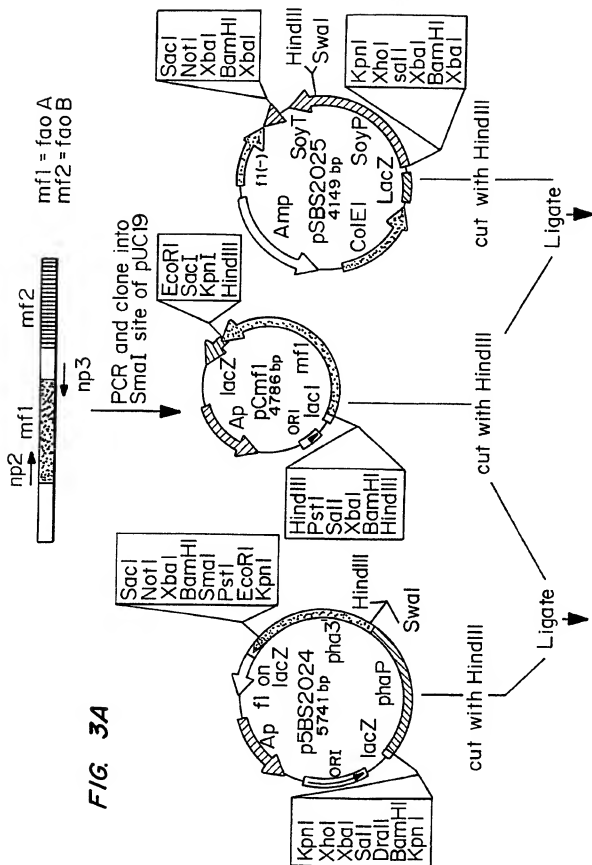
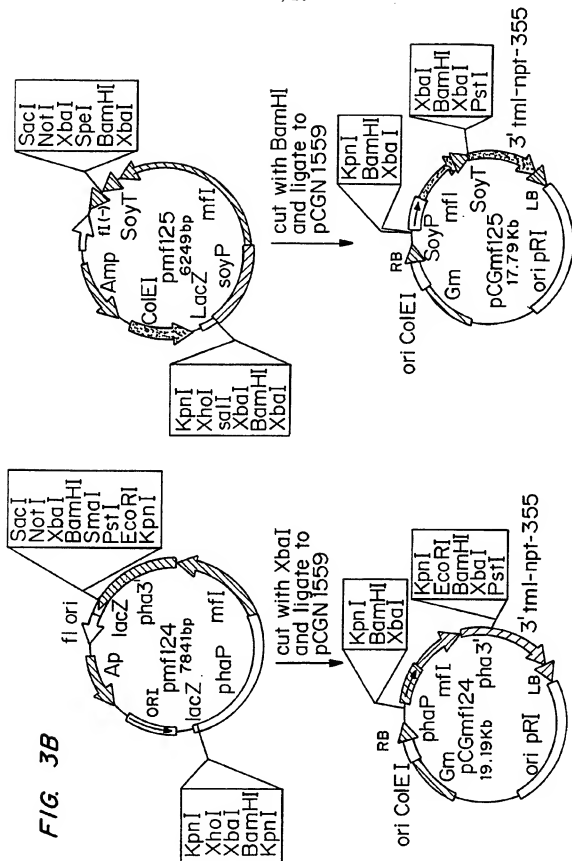


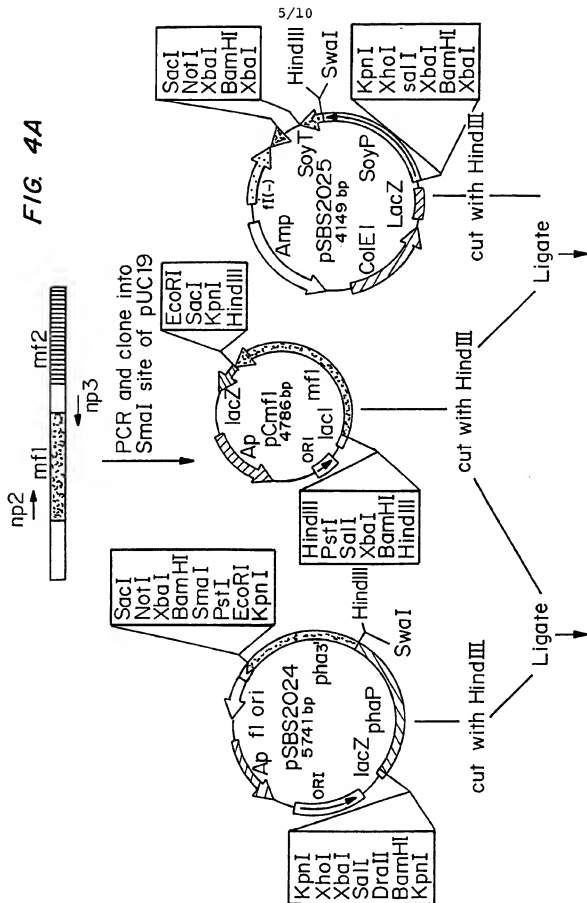
FIG. 2

3/10



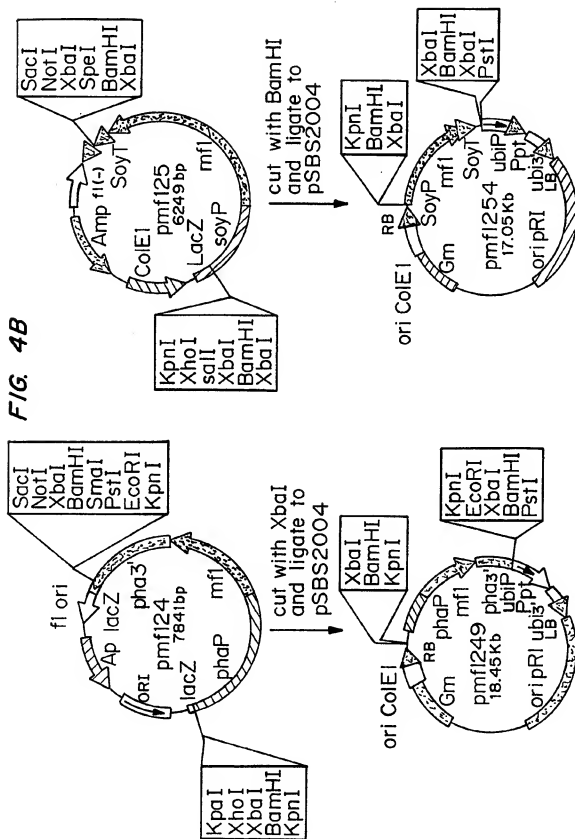
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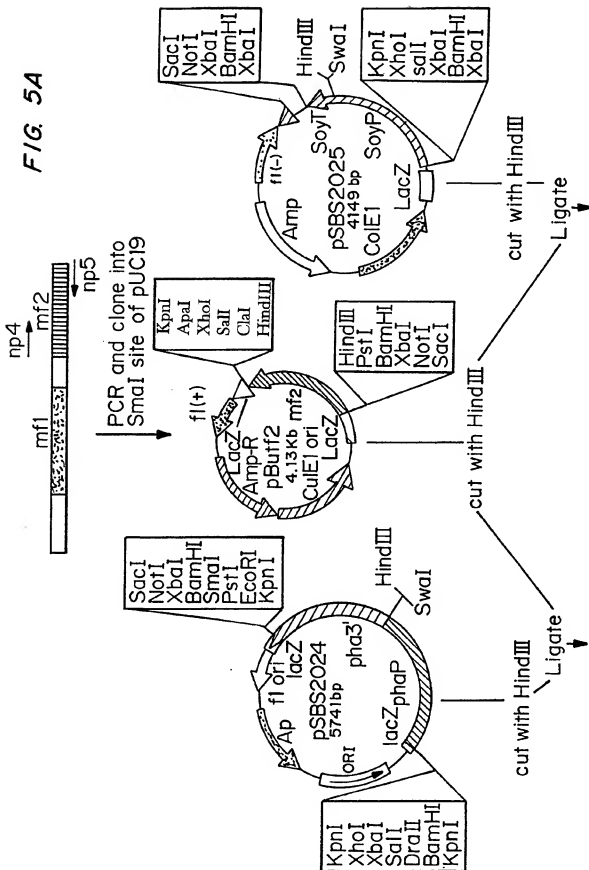


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FIG. 4B

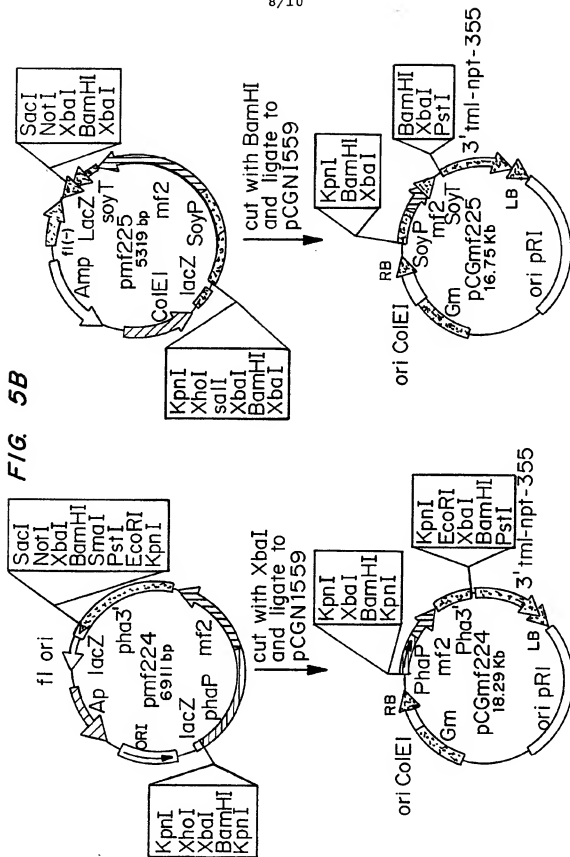


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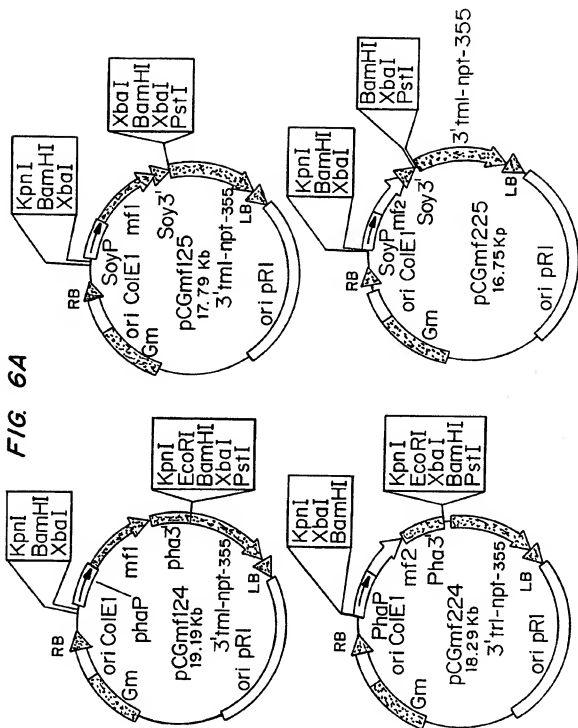
FIG. 5B





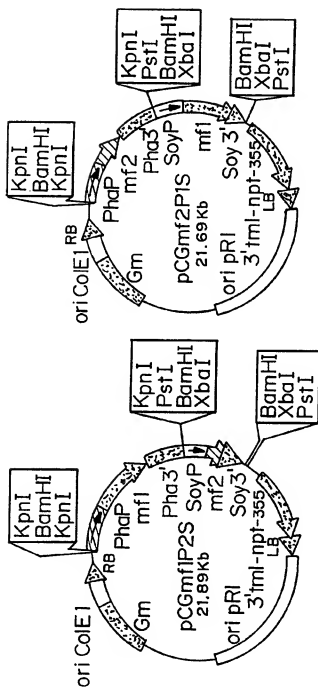
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FIG. 6A



10/10

FIG. 6B



## SEQUENCE LISTING

&lt;110&gt; Metabolix, Inc.

&lt;120&gt; Modification of Fatty Acid Metabolism in Plants

&lt;130&gt; MBX 024

&lt;140&gt;

&lt;141&gt;

&lt;150&gt; 60/077,107

&lt;151&gt; 1998-03-06

&lt;160&gt; 31

&lt;170&gt; PatentIn Ver. 2.0

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&lt;211&gt; 2703

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&lt;213&gt; Saccharomyces

&lt;220&gt;

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&lt;222&gt; (1)..(2703)

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 taa 2703

&lt;210&gt; 2

&lt;211&gt; 900

&lt;212&gt; PRT

&lt;213&gt; Saccharomyces

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1)..(900)

&lt;223&gt; fox2 encoded polypeptide

&lt;400&gt; 2

Met Pro Gly Asn Leu Ser Phe Lys Asp Arg Val Val Val Ile Thr Gly  
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Ala Gly Gly Gly Leu Gly Lys Val Tyr Ala Leu Ala Tyr Ala Ser Arg  
 20 25 30

Gly Ala Lys Val Val Val Asn Asp Leu Gly Gly Thr Leu Gly Gly Ser  
 35 40 45

Gly His Asn Ser Lys Ala Ala Asp Leu Val Val Asp Glu Ile Lys Lys  
 50 55 60  
 Ala Gly Gly Ile Ala Val Ala Asn Tyr Asp Ser Val Asn Glu Asn Gly  
 65 70 75 80  
 Glu Lys Ile Ile Glu Thr Ala Ile Lys Glu Phe Gly Arg Val Asp Val  
 85 90 95  
 Leu Ile Asn Asn Ala Gly Ile Leu Arg Asp Val Ser Phe Ala Lys Met  
 100 105 110  
 Thr Glu Arg Glu Phe Ala Ser Val Val Asp Val His Leu Thr Gly Gly  
 115 120 125  
 Tyr Lys Leu Ser Arg Ala Ala Trp Pro Tyr Met Arg Ser Gln Lys Phe  
 130 135 140  
 Gly Arg Ile Ile Asn Thr Ala Ser Pro Ala Gly Leu Phe Gly Asn Phe  
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 Gly Gln Ala Asn Tyr Ser Ala Ala Lys Met Gly Leu Val Gly Leu Ala  
 165 170 175  
 Glu Thr Leu Ala Lys Glu Gly Ala Lys Tyr Asn Ile Asn Val Asn Ser  
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 Ile Ala Pro Leu Ala Arg Ser Arg Met Thr Glu Asn Val Leu Pro Pro  
 195 200 205  
 His Ile Leu Lys Gln Leu Gly Pro Glu Lys Ile Val Pro Leu Val Leu  
 210 215 220  
 Tyr Leu Thr His Glu Ser Thr Lys Val Ser Asn Ser Ile Phe Glu Leu  
 225 230 235 240  
 Ala Ala Gly Phe Phe Gly Gln Leu Arg Trp Glu Arg Ser Ser Gly Gln  
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 Lys Trp Lys Glu Ile Thr Asp Tyr Arg Asp Lys Pro Phe Asn Lys Thr  
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 Gln His Pro Tyr Gln Leu Ser Asp Tyr Asn Asp Leu Ile Thr Lys Ala  
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Lys Lys Leu Pro Pro Asn Glu Gln Gly Ser Val Lys Ile Lys Ser Leu  
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 325 330 335  
 Ser His Ala Ile Trp Phe Ala Arg Tyr Gly Ala Lys Val Val Val Asn  
 340 345 350  
 Asp Ile Lys Asp Pro Phe Ser Val Val Glu Glu Ile Asn Lys Leu Tyr  
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 Gly Glu Gly Thr Ala Ile Pro Asp Ser His Asp Val Val Thr Glu Ala  
 370 375 380  
 Pro Leu Ile Ile Gln Thr Ala Ile Ser Lys Phe Gln Arg Val Asp Ile  
 385 390 395 400  
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 405 410 415  
 Lys Asp Glu Glu Trp Phe Ala Val Leu Lys Val His Leu Phe Ser Thr  
 420 425 430  
 Phe Ser Leu Ser Lys Ala Val Trp Pro Ile Phe Thr Lys Gln Lys Ser  
 435 440 445  
 Gly Phe Ile Ile Asn Thr Thr Ser Thr Ser Gly Ile Tyr Gly Asn Phe  
 450 455 460  
 Gly Gln Ala Asn Tyr Ala Ala Ala Lys Ala Ala Ile Leu Gly Phe Ser  
 465 470 475 480  
 Lys Thr Ile Ala Leu Glu Gly Ala Lys Arg Gly Ile Ile Val Asn Val  
 485 490 495  
 Ile Ala Pro His Ala Glu Thr Ala Met Thr Lys Thr Ile Phe Ser Glu  
 500 505 510  
 Lys Glu Leu Ser Asn His Phe Asp Ala Ser Gln Val Ser Pro Leu Val  
 515 520 525  
 Val Leu Leu Ala Ser Glu Glu Leu Gln Lys Tyr Ser Gly Arg Arg Val  
 530 535 540  
 Ile Gly Gln Leu Phe Glu Val Gly Gly Gly Trp Cys Gly Gln Thr Arg  
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Trp Gln Arg Ser Ser Gly Tyr Val Ser Ile Lys Glu Thr Ile Glu Pro  
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 Glu Glu Ile Lys Glu Asn Trp Asn His Ile Thr Asp Phe Ser Arg Asn  
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 Thr Ile Asn Pro Ser Ser Thr Glu Glu Ser Ser Met Ala Thr Leu Gln  
 595 600 605  
 Ala Val Gln Lys Ala His Ser Ser Lys Glu Leu Asp Asp Gly Leu Phe  
 610 615 620  
 Lys Tyr Thr Thr Lys Asp Cys Ile Leu Tyr Asn Leu Gly Leu Gly Cys  
 625 630 635 640  
 Thr Ser Lys Glu Leu Lys Tyr Thr Tyr Glu Asn Asp Pro Asp Phe Gln  
 645 650 655  
 Val Leu Pro Thr Phe Ala Val Ile Pro Phe Met Gln Ala Thr Ala Thr  
 660 665 670  
 Leu Ala Met Asp Asn Leu Val Asp Asn Phe Asn Tyr Ala Met Leu Leu  
 675 680 685  
 His Gly Glu Gln Tyr Phe Lys Leu Cys Thr Pro Thr Met Pro Ser Asn  
 690 695 700  
 Gly Thr Leu Lys Thr Leu Ala Lys Pro Leu Gln Val Leu Asp Lys Asn  
 705 710 715 720  
 Gly Lys Ala Ala Leu Val Val Gly Gly Phe Glu Thr Tyr Asp Ile Lys  
 725 730 735  
 Thr Lys Lys Leu Ile Ala Tyr Asn Glu Gly Ser Phe Phe Ile Arg Gly  
 740 745 750  
 Ala His Val Pro Pro Glu Lys Glu Val Arg Asp Gly Lys Arg Ala Lys  
 755 760 765  
 Phe Ala Val Gln Asn Phe Glu Val Pro His Gly Lys Val Pro Asp Phe  
 770 775 780  
 Glu Ala Glu Ile Ser Thr Asn Lys Asp Gln Ala Ala Leu Tyr Arg Leu  
 785 790 795 800  
 Ser Gly Asp Phe Asn Pro Leu His Ile Asp Pro Thr Leu Ala Lys Ala  
 805 810 815

Val Lys Phe Pro Thr Pro Ile Leu His Gly Leu Cys Thr Leu Gly Ile  
820 825 830

Ser Ala Lys Ala Leu Phe Glu His Tyr Gly Pro Tyr Glu Glu Leu Lys  
835 840 845

Val Arg Phe Thr Asn Val Val Phe Pro Gly Asp Thr Leu Lys Val Lys  
850 855 860

Ala Trp Lys Gln Gly Ser Val Val Val Phe Gln Thr Ile Asp Thr Thr  
865 870 875 880

Arg Asn Val Ile Val Leu Asp Asn Ala Ala Val Lys Leu Ser Gln Ala  
885 890 895

Lys Ser Lys Leu  
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<210> 3

<211> 2177

<212> DNA

<213> Artificial Sequence

<220>

<221> gene

<222> (1)..(2177)

<223> tetrafunctional beta-oxidation gene

<220>

<223> Description of Artificial Sequence

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gatatgtatg aacaagcctt gagaagagat gatgtgaagg caattgttgt tacagggtgca 180  
aagggaatat ttctgtgttg ctttgatata actgcttttg gtgtactcca aggaggaaag 240  
ggggagcaac caaatgttag aaacatatca attgaaatga tcaactgatat ttttgaagct 300  
gcccgaaaaa ctgcggttgc agcgatagat ggaactgtct ttgggtggagg gttggagggt 360  
gccatggctt gtcatgtctg aatatcaact cctaccgctc aattagggtt gcttgaactt 420  
cagctcggaa taattcctgg ttttggagga acacaacggc ttccacgtct tgggtgtctc 480  
tcaaaaggccc tagaaaatg gttgacgtca aagccaatta aaggacaaga agctcattct 540  
ttgggggttag tggatgccat tgtccctccc gaagagttga tcaacactgc acgtagatgg 600  
gtctttgaaa tcctagagcg gagaagacca tgggttcaca gtcttcacag gactgacaag 660  
ttagatgtct ttgctgaggc taggaaaata ttttaacttag ctagagctca ggcaagaaa 720  
cagtacccaa atcttaagca tacaattgcg tgcattgatg ctgttgaaac ggggtgtctc 780  
tctggccctc gtgctggact ttggaaggag gctgaagaat ttacagggact cctacattct 840  
gatacttgca aaagcttaat tcatatcttc ttgcccagc gttcaacaac taaggtagct 900



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 aaagaagtga agcataagtt ctctgcaggct ggcattgaca gactcagagc aaacctacaa 1080  
 agccgagtca aaaaagggaa tatgactaat gagaaattcg aaaagagtat ttctttactc 1140  
 aagggagttc ttaactacga aegtttttaa gatgtagata tggtagataga ggctgtttatt 1200  
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 aagaataata agaaaacacc agttgtcgtt ggaaattgta caggttttgc tgtcaacaga 1440  
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 cgtgtccttg ccgaaggcat agcagtcaaa gcagctgacc tggacattgc tgggtgtaag 1920  
 ggaatggggt tccccctcta cggggaggac tcatgttctg ggccgattct ctgggatcaa 1980  
 attacatcta ttcaagggtg gaggaatggt cgaacacgta tgggtgattt ttcaagccct 2040  
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 ctaaacctgc aatgtaagct catttcttta gtccgtgctc catcatgcgc ctattggaaa 2160  
 tgtccgtac caagcat 2177

&lt;210&gt; 4

&lt;211&gt; 725

&lt;212&gt; PRT

&lt;213&gt; Cucumber

&lt;220&gt;

&lt;221&gt; PEPTIDE

&lt;222&gt; (1) .. (725)

&lt;223&gt; tetrafunctional beta-oxidation protein

&lt;400&gt; 4

Met Gly Ser Asn Ala Lys Gly Arg Thr Val Met Glu Val Gly Thr Asp

1

5

10

15

Gly Val Ala Ile Ile Thr Ile Ile Asn Pro Pro Val Asn Ser Leu Ser

20

25

30

Phe Asp Val Leu Phe Ser Leu Arg Asp Ser Tyr Glu Gln Ala Leu Arg

35

40

45

Arg Asp Asp Val Lys Ala Ile Val Val Thr Gly Ala Lys Gly Lys Phe

50

55

60

Ser Gly Gly Phe Asp Ile Thr Ala Phe Gly Val Leu Gln Gly Gly Lys

65

70

75

80

Gly Glu Gln Pro Asn Val Arg Asn Ile Ser Ile Glu Met Ile Thr Asp  
 85 90 95  
 Ile Phe Glu Ala Ala Arg Lys Pro Ala Val Ala Ala Ile Asp Gly Leu  
 100 105 110  
 Ala Leu Gly Gly Gly Leu Glu Val Ala Met Ala Cys His Ala Arg Ile  
 115 120 125  
 Ser Thr Pro Thr Ala Gln Leu Gly Leu Pro Glu Leu Gln Leu Gly Ile  
 130 135 140  
 Ile Pro Gly Phe Gly Gly Thr Gln Arg Leu Pro Arg Leu Val Gly Leu  
 145 150 155 160  
 Ser Lys Ala Leu Glu Met Met Leu Thr Ser Lys Pro Ile Lys Gly Gln  
 165 170 175  
 Glu Ala His Ser Leu Gly Leu Val Asp Ala Ile Val Pro Pro Glu Glu  
 180 185 190  
 Leu Ile Asn Thr Ala Arg Arg Trp Ala Leu Glu Ile Leu Glu Arg Arg  
 195 200 205  
 Arg Pro Trp Val His Ser Leu His Arg Thr Asp Lys Leu Glu Ser Leu  
 210 215 220  
 Ala Glu Ala Arg Lys Ile Phe Asn Leu Ala Arg Ala Gln Ala Lys Lys  
 225 230 235 240  
 Gln Tyr Pro Asn Leu Lys His Thr Ile Ala Cys Ile Asp Ala Val Glu  
 245 250 255  
 Thr Gly Val Val Ser Gly Pro Arg Ala Gly Leu Trp Lys Glu Ala Glu  
 260 265 270  
 Glu Phe Gln Gly Leu Leu His Ser Asp Thr Cys Lys Ser Leu Ile His  
 275 280 285  
 Ile Phe Phe Ala Gln Arg Ser Thr Thr Lys Val Pro Gly Val Thr Asp  
 290 295 300  
 Leu Gly Leu Val Pro Arg Gln Ile Lys Lys Val Ala Ile Val Gly Gly  
 305 310 315 320  
 Gly Leu Met Gly Ser Gly Ile Ala Thr Ala Leu Ile Leu Ser Asn Tyr  
 325 330 335

His Val Val Leu Lys Glu Val Asn Asp Lys Phe Leu Gln Ala Gly Ile  
 340 345 350  
 Asp Arg Val Arg Ala Asn Leu Gln Ser Arg Val Lys Lys Gly Asn Met  
 355 360 365  
 Thr Asn Glu Lys Phe Glu Lys Ser Ile Ser Leu Leu Lys Gly Val Leu  
 370 375 380  
 Asn Tyr Glu Ser Phe Lys Asp Val Asp Met Val Ile Glu Ala Val Ile  
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 Glu Asn Val Ser Leu Lys Gln Gln Ile Phe Ser Asp Leu Glu Lys Tyr  
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 Cys Pro Pro His Cys Met Leu Ala Thr Asn Thr Ser Thr Ile Asp Leu  
 420 425 430  
 Glu Leu Ile Gly Glu Arg Ile Lys Ser Arg Asp Arg Ile Ile Gly His  
 435 440 445  
 Thr Ala Ala Gln Val Ile Val Asp Leu Leu Asp Val Gly Lys Asn Ile  
 450 455 460  
 Lys Lys Thr Pro Val Val Val Gly Asn Cys Thr Gly Phe Ala Val Asn  
 465 470 475 480  
 Arg Met Phe Phe Pro Tyr Ser Gln Ala Ala Ile Leu Leu Ala Glu His  
 485 490 495  
 Gly Val Asp Pro Tyr Gln Ile Asp Arg Ala Ile Ser Lys Phe Gly Met  
 500 505 510  
 Pro Met Gly Pro Phe Arg Leu Cys Asp Leu Val Gly Phe Gly Val Ala  
 515 520 525  
 Ala Ala Thr Ala Ser Gln Phe Val Gln Ala Phe Pro Glu Arg Thr Tyr  
 530 535 540  
 Lys Ser Met Leu Ile Pro Leu Met Gln Glu Asp Lys Asn Ala Gly Glu  
 545 550 555 560  
 Ser Thr Arg Lys Gly Phe Tyr Val Tyr Asp Lys Asn Arg Lys Ala Gly  
 565 570 575  
 Pro Asn Pro Glu Leu Lys Lys Tyr Ile Glu Lys Ala Arg Asn Ser Ser  
 580 585 590

Gly Val Ser Val Asp Pro Lys Leu Thr Lys Leu Pro Glu Lys Asp Ile  
 595 600 605  
 Val Glu Met Ile Phe Phe Pro Val Val Asn Glu Ala Cys Arg Val Leu  
 610 615 620  
 Ala Glu Gly Ile Ala Val Lys Ala Ala Asp Leu Asp Ile Ala Gly Val  
 625 630 635 640  
 Met Gly Met Gly Phe Pro Ser Tyr Arg Gly Gly Leu Met Phe Trp Ala  
 645 650 655  
 Asp Ser Leu Gly Ser Asn Tyr Ile Tyr Ser Arg Leu Glu Glu Trp Ser  
 660 665 670  
 Lys Gln Tyr Gly Gly Phe Phe Lys Pro Cys Gly Tyr Leu Ala Glu Arg  
 675 680 685  
 Ala Val Gln Gly Ala Thr Leu Ser Ala Pro Gly Gly His Ala Lys Pro  
 690 695 700  
 Arg Met Ala His Phe Phe Ser Pro Ala His Ile Met Pro Leu Leu Glu  
 705 710 715 720  
 Ile Val Arg Thr Lys  
 725

<210> 5

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
oligonucleotide primer- Primer 1

<400> 5

gatgggcgcg tccaagggtg g

21

<210> 6

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

## oligonucleotide primer- Primer 2

&lt;400&gt; 6

caaccggaag gtgccgccat t

21

&lt;210&gt; 7

&lt;211&gt; 3907

&lt;212&gt; DNA

<213> *Pseudomonas putida*

&lt;220&gt;

&lt;221&gt; gene

&lt;222&gt; (1) .. (3907)

&lt;223&gt; faoAB gene sequence

&lt;400&gt; 7

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 tgccaagtcg ccgctttgctg ttctgtctgc cagaaaaggc caggcaggcc gggttattca 180  
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&lt;210&gt; 8

&lt;211&gt; 27

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:

oligonucleotide primer- Primer GVR471

&lt;400&gt; 8

cggtaacctat tgaactccca gtatcat

27

&lt;210&gt; 9

<211> 27  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 oligonucleotide primer- Primer GVR472

<400> 9  
 catttaaata gtagagtatt gaatatg

27

<210> 10  
 <211> 1558  
 <212> DNA  
 <213> Bean Phaseolin

<220>  
 <221> promoter  
 <222> (1)..(1558)

<400> 10  
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 ttgttactttt aattttctcat aatctttggt tgaattatcc acgcttcgcc acacgatata 180  
 cctacaaaatt tattatttgg taaacatttt caaacccgat aaaattttat gaagtcocgt 240  
 ctatcttttaa tggtagcttaa cattttcata ttgaatatata taatttacct aatttttagcg 300  
 ttggttagaaa gcataaagat ttattcttat tcttctctcat ataatgttt aatatacaat 360  
 ataaacaaat tctttacctt aagaaggatt tcccatttta tattttaaaa atatatttat 420  
 caaatatttt tcaaccacgt aatcttcata ataataagt gtttcaaaag taataaaatt 480  
 taactccata atttttttat tcgactgac ttaaagcaac acccagtgac acaactagcc 540  
 atttttttct tgaataaaaa aaatccaatt atcattgtat ttttttata caatgaaaat 600  
 ttacaccaac aatcatttgt ggtatttctg aagcaagtca tggttatgcaa aattctataa 660  
 ttcccatlgt acactacgga agtaactgaa gatctgcttt tacatgcgag acacatcttc 720  
 taaagtaatt ttaataatag ttactatatt caagatttca tatatcaaat actcaatatt 780  
 acttctaaaa aattaattag atataattaa aatattacct ttttaatttt aagtttaatt 840  
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 taaagtaaat ataagtaatg tagtagagtg tttagtggtt accctaaac ataacata 960  
 acattatttg tggactaatt ttcatatatt tcttattgct ttacctttt cttggtatgt 1020  
 aagtcogtaa ctagaattac agtgggttgc catggcactc tgtggtcttt tggttcatgc 1080  
 atgggtcttg cgcaagaaaa agacaaagaa caaagaaaa agacaaaaca gagagacaaa 1140  
 acgcaatcac caaaccaact caaattagtc actggctgat caagatcgcc gcgtccatgt 1200  
 atgtcttaatt gccatgcaaa gcaacacgtg cttaacatgc actttaaatg gctcaccat 1260  
 ctcaaccac acacaaacac attgcctttt tcttcatcat caccacaacc acctgtatat 1320  
 attcatcttc ttccgccacc tcaattttct cacttcaaca caggtcaacc tgeatattgcg 1380  
 tgcacatcca tgcccaaatc tccatgcatg ttcccaaccac cttctctctt atataatacc 1440  
 tataaatacc tctaattatca ctcaacttct tcatcatcca tccatccaga gtactactac 1500  
 tctactacta taatacccca acccaactca tattcaatc tactctacta ttttaattg 1558

<210> 11  
 <211> 983  
 <212> DNA  
 <213> Soybean oleosin

<220>  
 <221> promoter  
 <222> (1)..(983)

<400> 11  
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 tctgtcaaat gccatttggt gttgaaataa agtaacttat gcatcaattt aaaacaatca 180  
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 gttgagacat tgactattgt gtgctatttc aaaaagatct gataaaatat ttaataaaac 300  
 attaaaagta aataataatc gctaaacatc atcaaaatat taatcattag attcaatttt 360  
 tgcaattaaa accagaagaa ctaaatctac attaccatcc ttaagactat acatagagaa 420  
 ttaactttaa tgttatattt aaggaaaagg acgaacctta aaacttaaat acaattgtat 480  
 gattaatttt agtattgtct ttaatgagaa tttaagtttt attcactaat ttatgattat 540  
 ttcatttact aatttatgta atgtgatttc aataagtgag gtaactccg attgattgaa 600  
 gataccacca acaccaacac caccaccacc tgcgaaactg tacgtatctc aattgtcctt 660  
 aataaaaatg taaatagtag attattctcc ttgctgtgta ttattttatg gcccccagct 720  
 ttaatttttc tgaatgactt aacccagggc aaactgaaac atgttctctc tgcaaaagccc 780  
 caactcatca tgcattcatg acgtgtcatc atccagcaac tccacttttg ctatatnaact 840  
 cctcccccat cacactcccc atctctctaa cacacacata cccccacta acaataattc 900  
 ctccacttgc agaacttagt tctctgttgc atcatcatca tcttcattag tgttagccct 960  
 aacttcacct taaccattta atg 983

<210> 12  
 <211> 38  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 oligonucleotide primer- Primer JA408

<400> 12  
 tctagatata tccatttctt aatataatcc tcttattc 38

<210> 13  
 <211> 30  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:  
 oligonucleotide primer- npl



<400> 13  
catttaaatg gttaaggtga aggtagggt  
30

<210> 14  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide primer- Primer np2

<400> 14  
aagcttaaaa tgatttacga aggtaaagcc  
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<210> 15  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide primer- Primer np3

<400> 15  
attgctttca gttgaagcgc tg  
22

<210> 16  
<211> 30  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide primer- Primer np4

<400> 16  
aagcttaaaa tgagcctgaa tocaagagac  
30

<210> 17  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide primer- Primer np5

<400> 17  
aaagtttcag acgcgttcga agacagtg 28

<210> 18  
<211> 56  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide primer- Primer N-fox2b

<400> 18  
tcccccgga ggaggttttt attatgcctg gaaatttatt cttcaaagat agagt 56

<210> 19  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide primer- Primer N-bamfox2b

<400> 19  
aaggatcctt gatgtcattt acaactacc 29

<210> 20  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide primer- Primer C-fox2

<400> 20  
gctctagata gggaagatg tatgtaag 28

<210> 21  
<211> 19  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide primer- Primer C-bamfox2

<400> 21  
tgacatcaag gatcctttt 19

<210> 22  
<211> 39  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide primer- Primer GVR396

<400> 22  
gatttaaatg caagcttaaa taagtatgaa ctaaaatgc 39

<210> 23  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:  
oligonucleotide primer- Primer GVR397

<400> 23  
cggtagctta gttggtaggg tgcta 25

<210> 24  
<211> 2162  
<212> DNA  
<213> *Pseudomonas putida*

<220>  
<221> gene  
<222> (1)..(2162)  
<223> *FacA* gene sequence

<400> 24  
aagcttaaat gatttacgaa ggtaaagcca tcacggttaa ggctcttgaa agtggcatcg 60  
tcgagctcaa gttcgacctc aagggtgagt ccgtcaacaa gttcaaccgc cttaccctga 120  
acgagctgcg ccaggccgtc gatgccatcc gggccgatgc ttcggtcaag ggcgtgatcg 180  
tcaggagtgg caaggacgtg ttcacgtcgc gcgccgacat caccgagttc gtcgacaaat 240  
tcaagctgcc tgaggccgaa ctggtcgcgc gcaacctgga agccaatcgc atcttcaacg 300  
cgttcgaaga cctcgaagtg ccgaccgttg ccgccatcaa cggcatcgcg ctgggcggcg 360  
gcctggaaat gtgctggcg gccgactacc gggtcatgtc caccagcgcc aggatcggcc 420  
tgccggaagt caagctgggt atctacccgg gctttggcgg taccgtcgcc ctgcccgccc 480  
tgatcggtcc ggacaacgcc atcgagtgga tcgccgccgg caaggaaaac cgtgccgaag 540

atgccctgaa agtggggggcc gtccagcgcc tggctgcccc tgaactgctg ctggccgggtg 600  
 ccctcgacct gatcaagcgt gccatcagtg gcgagctgga ctacaaggcc aagcgccagc 660  
 cgaagctgga aaagctcaag ctcaatgcc tccagcagat gatggccttc gagactgcca 720  
 agggctctgt cgtggccag gccggcccg actaccggc ccgggtcgaa gcgatcaaga 780  
 gcatccagaa agccgccaac ttgggtcgcg acaaggccct ggaagtcgaa gccgcaggct 840  
 ttgccaaact ggccaagacc ttgtcgccg agagcctgat cggcttgctc ctcaacgact 900  
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 accgcaccgc caagctcggt gaattggcca agaaccggca gcgcttcttc aactgaaagc 2160  
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2162

&lt;210&gt; 25

&lt;211&gt; 1190

&lt;212&gt; DNA

<213> *Pseudomonas putida*

&lt;220&gt;

&lt;221&gt; gene

&lt;222&gt; (1) .. (1190)

<223> *FaoB* gene sequence

&lt;400&gt; 25

aagcttaaat gagcctgaat ccaagagacg tgggtgattg cgacttcggt cgcacgcca 60  
 tgggcccgtc caagggctggc atgcaccgca acaccgcgc cgaagacatg tcggcgacc 120  
 tgaacagcaa gctcgtgaa gcgaacggca aggtcgaccc gaaagaagtc gaggacgtga 180  
 tctggggctg cgtcaaccag accctggagc agggctggaa catcgccgc atggcttcgc 240  
 tgatgacccc gatccgcac aactctgcgg cgcagacgt cagccgcctg tggcgctcgt 300  
 ccacgagcgc gctgcacac gccgccagg cgatcatgac cggtaacggt gatgtgttcg 360  
 tggctcgtgg cgtggagcac atgggcccag tcagcatgat gcatggcgta gaccocacc 420  
 cgcacctgtc cttgatgcc gccaaaggct ccgggatgat gggcctgact gcagaaatgc 480

tcggcgaagt gcacggcctc acccgtgagc agcaggacct gttcggettgc cgttcgcacc 540  
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 ccaccctcga aggcctggca tcgctcaagc ctgcgttcaa ccgaaaggc ggtacggta 720  
 cggcgggtac ctgctgcgag atcaccgacg gcgctcgtg catgatcgtc atgtccggtc 780  
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 gtgtcgaccc ggcaatcatg ggctacggcc cggtgccatc gacccgaaa gccctcaagc 900  
 gtgggggctt gaccatggcc gatctcgact tcctcgagct caacgaagcc ttcgctgcgc 960  
 aggcctcgtc cgtgctgaaa gacttgaaag tgcctcgacaa gatggatgag aaggttaac 1020  
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 gcaccctcgt caacgtcatg aagcaaaatg gcggtacgt ggggtgttgcg accatgtgcg 1140  
 tcggcctggg ccaaggctac accactgtct tcgaacgcgt ctgaaagctt 1190

<210> 26

<211> 391

<212> PRT

<213> *Pseudomonas putida*

<220>

<221> PEPTIDE

<222> (1)..(391)

<223> *FaoB* amino acid sequence

<400> 26

Met Ser Leu Asn Pro Arg Asp Val Val Ile Val Asp Phe Gly Arg Thr  
 1 5 10 15

Pro Met Gly Arg Ser Lys Gly Gly Met His Arg Asn Thr Arg Ala Glu  
 20 25 30

Asp Met Ser Ala His Leu Ile Ser Lys Leu Leu Glu Arg Asn Gly Lys  
 35 40 45

Val Asp Pro Lys Glu Val Glu Asp Val Ile Trp Gly Cys Val Asn Gln  
 50 55 60

Thr Leu Glu Gln Gly Trp Asn Ile Ala Arg Met Ala Ser Leu Met Thr  
 65 70 75 80

Pro Ile Pro His Thr Ser Ala Ala Gln Thr Val Ser Arg Leu Cys Gly  
 85 90 95

Ser Ser Met Ser Ala Leu His Thr Ala Ala Gln Ala Ile Met Thr Gly  
 100 105 110

Asn Gly Asp Val Phe Val Val Gly Gly Val Glu His Met Gly His Val  
 115 120 125

Ser Met Met His Gly Val Asp Pro Asn Pro His Leu Ser Leu His Ala  
 130 135 140

Ala Lys Ala Ser Gly Met Met Gly Leu Thr Ala Glu Met Leu Gly Lys  
 145 150 155 160

Met His Gly Ile Thr Arg Glu Gln Gln Asp Leu Phe Gly Leu Arg Ser  
 165 170 175

His Gln Leu Ala His Lys Ala Thr Val Glu Gly Lys Phe Lys Asp Glu  
 180 185 190

Ile Ile Pro Met Gln Gly Tyr Asp Glu Asn Gly Phe Leu Lys Val Phe  
 195 200 205

Asp Phe Asp Glu Thr Ile Arg Pro Glu Thr Thr Leu Glu Gly Leu Ala  
 210 215 220

Ser Leu Lys Pro Ala Phe Asn Pro Lys Gly Gly Thr Val Thr Ala Gly  
 225 230 235 240

Thr Ser Ser Gln Ile Thr Asp Gly Ala Ser Cys Met Ile Val Met Ser  
 245 250 255

Gly Gln Arg Ala Met Asp Leu Gly Ile Gln Pro Leu Ala Val Ile Arg  
 260 265 270

Ser Met Ala Val Ala Gly Val Asp Pro Ala Ile Met Gly Tyr Gly Pro  
 275 280 285

Val Pro Ser Thr Gln Lys Ala Leu Lys Arg Ala Gly Leu Thr Met Ala  
 290 295 300

Asp Ile Asp Phe Ile Glu Leu Asn Glu Ala Phe Ala Ala Gln Ala Leu  
 305 310 315 320

Pro Val Leu Lys Asp Leu Lys Val Leu Asp Lys Met Asp Glu Lys Val  
 325 330 335

Asn Leu His Gly Gly Ala Ile Ala Leu Gly His Pro Phe Gly Cys Ser  
 340 345 350

Gly Ala Arg Ile Ser Gly Thr Leu Leu Asn Val Met Lys Gln Asn Gly  
 355 360 365

Gly Thr Leu Gly Val Ala Thr Met Cys Val Gly Leu Gly Gln Gly Ile  
 370 375 380

Thr Thr Val Phe Glu Arg Val

385

390

&lt;210&gt; 27

&lt;211&gt; 1244

&lt;212&gt; DNA

&lt;213&gt; Bean Phaseolin

&lt;220&gt;

&lt;221&gt; terminator

&lt;222&gt; (1)..(1244)

&lt;400&gt; 27

gatttaaatg caagcttaaa taagtatgaa ctaaaatgca thtaggtgta agagctcatg 60  
 gagagcatgg aatattgtat ccgaccatgt aacagtataa taactgagct ccatctcact 120  
 tctcttatga ataaacaaag gatgttatga tatattaaca ctctatctat gcaccttatt 180  
 gttctatgat aaattctctc ttattattat aaatcatctg aatcgtgacg gcttatggaa 240  
 gtcttcaaat agtacaaaaa caaatgtgta ctataagact ttctaaacaa ttctaaacttt 300  
 agcattgtga acgagacata agtgtaaga agacataaca attataatgg aagaagtttg 360  
 tctccattta tatattatat attaccact tatgtattat attaggatgt taaggagaca 420  
 taacaattat aaagagagaa gtttgtatcc atttatatat tatatactac ccattttat 480  
 ttataactta tccacttatt taatgtcttt ataaggtttg atccatgata ttctataat 540  
 tttagttgat atgtatatga aagggtacta ttgtaactct cttaactctgt ataaaggttg 600  
 gatcatcctt aaagtgggtc tatttaattt tattgcttct tacagataaa aaaaaaatta 660  
 tgagttgggt tgataaaata ttgaaggatt taaaataata ataaataata aatacatat 720  
 aatataatga tataaattta ttataatata acatttatct ataaaaaagt aaatattgtc 780  
 ataaatctat acaatcgttt agccttgctg gacgactctc aattatttaa acgagagtaa 840  
 acatatttga ctttttggtt atttaacaaa ttattattta acactatag aaattttttt 900  
 tttttatcgg caaggaaata aaattaattt agggaggaca atggtgtgtc ccaatcctta 960  
 tacaaaccaac ttccacagga aggtcaggtc ggggacaaca aaaaaacagg caagggaat 1020  
 tttttatttt ggggtgtctt gtttgtgcga taatttatgc agtaaaacac tacacataac 1080  
 ccttttagca gttagagcaat ggttgaccgt gtgcttagct tctttttattt tattttttta 1140  
 tcagcaaga ataaataaaa taaaatgaga cacttcaggg atgtttcaac ccttatacca 1200  
 aaccccaaaa acaagtttcc tagcacccta ccaactaagg tacc 1244

&lt;210&gt; 28

&lt;211&gt; 225

&lt;212&gt; DNA

&lt;213&gt; Soybean oleosin

&lt;220&gt;

&lt;221&gt; terminator

&lt;222&gt; (1)..(225)

&lt;400&gt; 28

aagcttacgt gatgagtatt aatgtgttgt tatgaactta tgaatgttgt ttatgtgggg 60  
 aataaataga tgaatgtacc tcttcttgcc tatgtagtag gtttgggtgt ttgtgtgtct 120

agcttttgctt atttagtaat tagtagaagg gatgttcgtt cgtgtctcat aaaaaggggt 180  
actaccactc tggcaatgtg atttgtattt gatgaattgt ctaga 225

<210> 29

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
oligonucleotide primer- Primer JA410

<400> 29

aagcttacgt gatgagtatt aatgtgttgt tatg 34

<210> 30

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:  
oligonucleotide primer- Primer JA411

<400> 30

tctagacaat tcatcaaata caaatcacat tgcc 34

<210> 31

<211> 715

<212> PRT

<213> Pseudomonas putida

<220>

<221> PEPTIDE

<222> (1)..(715)

<223> FaoA amino acid sequence

<400> 31

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Ile	Val	Glu	Leu	Lys	Phe	Asp	Leu	Lys	Gly	Glu	Ser	Val	Asn	Lys	Phe
		20					25						30		

Asn	Arg	Leu	Thr	Leu	Asn	Glu	Leu	Arg	Gln	Ala	Val	Asp	Ala	Ile	Arg
		35					40					45			

Ala	Asp	Ala	Ser	Val	Lys	Gly	Val	Ile	Val	Arg	Ser	Gly	Lys	Asp	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----



50					55					60					
Phe	Ile	Val	Gly	Ala	Asp	Ile	Thr	Glu	Phe	Val	Asp	Asn	Phe	Lys	Leu
65					70					75					80
Pro	Glu	Ala	Glu	Leu	Val	Ala	Gly	Asn	Leu	Glu	Ala	Asn	Arg	Ile	Phe
				85						90				95	
Asn	Ala	Phe	Glu	Asp	Leu	Glu	Val	Pro	Thr	Val	Ala	Ala	Ile	Asn	Gly
			100					105					110		
Ile	Ala	Leu	Gly	Gly	Gly	Leu	Glu	Met	Cys	Leu	Ala	Ala	Asp	Tyr	Arg
			115				120						125		
Val	Met	Ser	Thr	Ser	Ala	Arg	Ile	Gly	Leu	Pro	Glu	Val	Lys	Leu	Gly
					135							140			
Ile	Tyr	Pro	Gly	Phe	Gly	Gly	Thr	Val	Arg	Leu	Pro	Arg	Leu	Ile	Gly
145				150						155				160	
Ser	Asp	Asn	Ala	Ile	Glu	Trp	Ile	Ala	Ala	Gly	Lys	Glu	Asn	Arg	Ala
			165					170						175	
Glu	Asp	Ala	Leu	Lys	Val	Gly	Ala	Val	Asp	Ala	Val	Val	Ala	Pro	Glu
			180				185						190		
Leu	Leu	Leu	Ala	Gly	Ala	Leu	Asp	Leu	Ile	Lys	Arg	Ala	Ile	Ser	Gly
			195				200					205			
Glu	Leu	Asp	Tyr	Lys	Ala	Lys	Arg	Gln	Pro	Lys	Leu	Glu	Lys	Leu	Lys
			210				215					220			
Leu	Asn	Ala	Ile	Glu	Gln	Met	Met	Ala	Phe	Glu	Thr	Ala	Lys	Gly	Phe
225				230						235				240	
Val	Ala	Gly	Gln	Ala	Gly	Pro	Asn	Tyr	Pro	Ala	Pro	Val	Glu	Ala	Ile
				245					250					255	
Lys	Ser	Ile	Gln	Lys	Ala	Ala	Asn	Phe	Gly	Arg	Asp	Lys	Ala	Leu	Glu
			260					265					270		
Val	Glu	Ala	Ala	Gly	Phe	Ala	Lys	Leu	Ala	Lys	Thr	Ser	Val	Ala	Glu
			275				280					285			
Ser	Leu	Ile	Gly	Leu	Phe	Leu	Asn	Asp	Gln	Glu	Leu	Lys	Arg	Lys	Ala
			290				295					300			
Lys	Ala	His	Asp	Glu	Ile	Ala	His	Asp	Val	Lys	Gln	Ala	Ala	Val	Leu

305	310	315	320
Gly Ala Gly Ile Met Gly Gly Gly Ile Ala Tyr Gln Ser Ala Val Lys			
325		330	335
Gly Thr Pro Ile Leu Met Lys Asp Ile Arg Glu Glu Ala Ile Gln Leu			
340	345		350
Gly Leu Asn Glu Ala Ser Lys Leu Leu Gly Asn Arg Val Glu Lys Gly			
355	360		365
Arg Leu Thr Pro Ala Lys Met Ala Glu Ala Leu Asn Ala Ile Arg Pro			
370	375	380	
Thr Leu Ser Tyr Gly Asp Phe Ala Asn Val Asp Ile Val Val Glu Ala			
385	390	395	400
Val Val Glu Asn Pro Lys Val Lys Gln Ala Val Leu Ala Glu Val Glu			
405	410		415
Gly Gln Val Lys Asp Asp Ala Ile Leu Ala Ser Asn Thr Ser Thr Ile			
420	425		430
Ser Ile Asn Leu Leu Ala Lys Ala Leu Lys Arg Pro Glu Asn Phe Val			
435	440		445
Gly Met His Phe Phe Asn Pro Val His Met Met Pro Leu Val Glu Val			
450	455		460
Ile Arg Gly Glu Lys Ser Ser Asp Val Ala Val Ala Thr Thr Val Ala			
465	470	475	480
Tyr Ala Lys Lys Met Gly Lys Asn Pro Ile Val Val Asn Asp Cys Pro			
485	490		495
Gly Phe Leu Val Asn Arg Val Leu Phe Pro Tyr Phe Gly Gly Phe Ala			
500	505		510
Lys Leu Val Ser Ala Gly Val Asp Phe Val Arg Ile Asp Lys Val Met			
515	520		525
Glu Lys Phe Gly Trp Pro Met Gly Pro Ala Tyr Leu Met Asp Val Val			
530	535		540
Gly Ile Asp Thr Gly His His Gly Arg Asp Val Met Ala Glu Gly Phe			
545	550	555	560
Pro Asp Arg Met Lys Asp Glu Arg Arg Ser Ala Val Asp Ala Leu Tyr			

565					570					575						
Glu	Ala	Asn	Arg	Leu	Gly	Gln	Lys	Asn	Gly	Lys	Gly	Phe	Tyr	Ala	Tyr	
580					585					590						
Glu	Thr	Asp	Lys	Arg	Gly	Lys	Pro	Lys	Lys	Val	Phe	Asp	Ala	Thr	Val	
595					600					605						
Leu	Asp	Val	Leu	Lys	Pro	Ile	Val	Phe	Glu	Gln	Arg	Glu	Val	Thr	Asp	
610					615					620						
Glu	Asp	Ile	Ile	Asn	Trp	Met	Met	Val	Pro	Leu	Cys	Leu	Glu	Thr	Val	
625					630					635					640	
Arg	Cys	Leu	Glu	Asp	Gly	Ile	Val	Glu	Thr	Ala	Ala	Glu	Ala	Asp	Met	
645					650					655						
Gly	Leu	Val	Tyr	Gly	Ile	Gly	Phe	Pro	Pro	Phe	Arg	Gly	Gly	Ala	Leu	
660					665					670						
Arg	Tyr	Ile	Asp	Ser	Ile	Gly	Val	Ala	Glu	Phe	Val	Ala	Leu	Ala	Asp	
675					680					685						
Gln	Tyr	Ala	Asp	Leu	Gly	Pro	Leu	Tyr	His	Pro	Thr	Ala	Lys	Leu	Arg	
690					695					700						
Glu	Met	Ala	Lys	Asn	Gly	Gln	Arg	Phe	Phe	Asn						
705					710					715						

# INTERNATIONAL SEARCH REPORT

International Application No  
PCT/US 99/04999

**A. CLASSIFICATION OF SUBJECT MATTER**  
IPC 6 C12N15/52 C12N15/82 A01H5/00

According to International Patent Classification (IPC) or to both national classification and IPC

## B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)  
IPC 6 C12N A01H

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

## C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category \* Citation of document, with indication, where appropriate, of the relevant passages

Relevant to claim No.

X DENG W L ET AL: "EXPRESSION OF SOYBEAN-EMBRYO LIPOXYGENASE-2 IN TRANSGENIC TOBACCO TISSUE" PLANTA, (MAY 1992) VOL. 187, NO. 2, PP. 203-208. ISSN: 0032-0935., XP002108604 UNIV KENTUCKY, DEPT AGRON, LEXINGTON, KY, 40546; UNIV KENTUCKY, DEPT HORT & LANDSCAPE ARCHITECTURE, LEXINGTON, KY, 40546 the whole document  
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10,13,  
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8 January 1998 (1998-01-08)  
  
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☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

### \* Special categories of cited documents:

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\*O\* document referring to an oral disclosure, use, exhibition or other means

\*P\* document published prior to the international filing date but later than the priority date claimed

\*T\* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention

\*X\* document of particular relevance: the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone

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\*A\* document member of the same patent family

Date of the actual completion of the international search

Date of mailing of the international search report

8 July 1999

21/07/1999

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## INTERNATIONAL SEARCH REPORT

 Int'l Application No.  
 PCT/US 99/04999

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A	<p>ISHIKAWA M. ET AL.: "Reconstitution, morphology and crystallization of a fatty acid beta-oxidation multienzyme complex from Pseudomonas fragi"            BIOCHEMICAL JOURNAL, vol. 328, 1997, pages 815-820, XP002108606            the whole document</p>	1-24
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A	<p>WO 98 06854 A (MONSANTO CO)            19 February 1998 (1998-02-19)            see esp. ex.10</p>	1-24
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## INTERNATIONAL SEARCH REPORT

Int'l Application No  
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## C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
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